

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:37:39 ; Search time 78.6609 Seconds

(without alignments)
1323.818 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1332

Sequence: 1 MKLPLRLVLMFWIPASSD.....EVTHQGLSSPVTKSFNRGEC 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1232	100.0	237	9	ADU70077 Mouse/hum
2	1175.5	95.4	238	2	AAW14937 Murine an
3	1175.5	95.4	238	2	AAW14942 3F4 Human
4	1164.5	94.5	238	6	ABP58288 Humanised
5	1113.5	90.4	238	6	AAU07744 Humanised
6	1113.5	90.4	238	6	ABR39842 Humanised
7	1106	89.8	238	8	ADS88785 Sequence
8	1103.5	89.6	219	8	ADP84971 Chimeric
9	1094	88.8	239	2	AAW71876 Anti-huma
10	1094	88.8	239	2	AAW71876 Anti-huma
11	1091	88.6	239	2	AAW71878 Anti-huma
12	1091	88.6	239	2	AAW71878 Anti-huma
13	1090	88.5	239	2	AAW71877 Anti-huma
14	1090	88.5	239	2	AAW71877 Anti-huma
15	1089.5	88.4	219	9	ADW77072 Light Cha
16	1087	88.2	239	2	AAW71879 Anti-huma
17	1087	88.2	239	2	AAW71879 Anti-huma
18	1086.5	88.2	219	8	ADP84971 Chimeric
19	1068.5	86.8	219	8	ADP84971 Chimeric
20	1049	85.1	239	9	ABE45871 Human mon
21	1046	84.9	239	9	ABE45871 Human mon
22	1043	84.7	239	9	ABE45871 Human mon
23	1043	84.7	239	9	ABE45871 Human mon
24	1043	84.7	242	2	AAW63762 Macaque p

25	1043	84.7	242	2	AAW23790 Chimeric
26	1043	84.7	242	2	AAW31580 Chimeric
27	1043	84.7	242	2	AAW42323 Murine va
28	1043	84.7	242	2	AAW33745 Chimeric
29	1043	84.7	242	2	AAW63311 Anti-IL-8
30	1043	84.7	242	2	AAW40126 Chimeric
31	1043	84.7	242	2	AAW29442 Chimeric
32	1043	84.7	242	2	AAW77748 Chimeric
33	1043	84.7	242	2	AAW30305 Murine 6G
34	1043	84.7	242	2	ABU13782 Mouse ant
35	1043	84.7	242	2	ABU59495 Mouse ant
36	1043	84.7	242	2	ABE39078 Murine 6G
37	1039	84.3	239	7	AAW28421 Human ant
38	1036	84.1	239	3	AAW82617 Human ant
39	1032	83.8	239	7	AAW28461 Human ant
40	1030	83.6	220	8	ADP42960 Humanised
41	1030	83.6	220	8	ADP42960 Humanised
42	1030	83.6	239	3	AAW82611 Human HUI
43	1030	83.6	239	7	ADP28465 Human ant
44	1029	83.5	239	2	AAW01819 Primatiae
45	1029	83.5	239	2	AAW63762 Macaque p

ALIGNMENTS

RESULT 1	ADU70077	ADU70077 standard; protein; 237 AA.
XX	ADU70077;	
AC	ADU70077;	
XX	24-FEB-2005 (first entry)	
DT		
XX	Mouse/human chimeric monoclonal antibody 6B5 light chain, SEQ:16.	
DE	Antibody engineering; chimeric antibody; drug dependence; phenylalidine;	
XX	PCP; antidiabetic; toxicity; toxicity and intoxication;	
KW	psychiatric disorder; immunoglobulin; chimeric monoclonal antibody 6B5;	
KM	ch-mab6B5; light chain.	
XX		
XX	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
XX	US2004242848-A1.	
FN		
XX	02-DEC-2004.	
PD		
XX	21-APR-2004; 2004US-00828782.	
PF		
XX	21-APR-2003; 2003US-0464190P.	
FR		
XX	(OWEN/) OWENS S M.	
PA	(LACY/) LACY H M.	
XX		
PI	Owens SM, Lacy HM;	
XX	WPI; 2005-011672/01.	
DR	N-PSDB; ADU70076.	
DR		
XX	New chimeric mouse/human monoclonal antibody for treating phenylalidine	
PT	drug abuse and toxicity comprises human immunoglobulin constant domains	
PT	and immunoglobulin variable domains of murine antibody.	
XX		
PS	Claim 4; SEQ ID NO 16; 34P; English.	
XX		
CC	The invention relates to a chimeric mouse/human monoclonal antibody named	
CC	ch-mab6B5 (see ADU70077 and ADU70079) which is specific for phenylalidine	
CC	(PCP). ch-mab6B5 comprises immunoglobulin constant domains of human	
CC	origin and immunoglobulin variable domains from the murine anti-PCP	
CC	monoclonal antibody 6B5. The invention also relates to DNA sequences	
CC	encoding the light and heavy chains of the chimeric antibody (ADU70076	

CC and ADU70078 respectively); to expression vectors and mammalian or plant
 CC host cells comprising either of these DNA sequences; the recombinant
 CC production of the chimeric antibody; a pharmaceutical composition
 CC comprising the chimeric antibody; and a method of treating
 CC arylcyclohexylamine drug abuse using the chimeric antibody. The chimeric
 CC antibody reverses and/or reduces the adverse effects of
 CC arylcyclohexylamine drug abuse. The chimeric antibody, compositions
 CC comprising it and method of the invention are useful for treating abuse
 CC and toxicity of the arylcyclohexylamine class of drugs such as PCP, 1-(1-
 CC (2-chienyl) cyclohexyl) piperidine (TCP) and N-ethyl-1-
 CC phenylcyclohexylamine (PCB) or other structurally similar, psychoactive
 CC analogs. The present sequence represents the chimeric light chain of ch-
 CC mAb85.

CC Sequence 237 AA;

Query Match 100.0%; Score 1232; DB 9; Length 237;
 Best Local Similarity 100.0%; Pred. No. 3.2e-69;
 Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRLPVRLVLMFWIPASSSDVMTQTPLSLPVLSDQASISCRSSQTIYHSNGNTYLEMY 60
 DB 1 MRLPVRLVLMFWIPASSSDVMTQTPLSLPVLSDQASISCRSSQTIYHSNGNTYLEMY 60
 QY 61 LQKPGQSPKLLIYKYSNRFSGVDPDRFSGSGSTDTLTLSRYEADLVGYTCFQGTTHAPY 120
 DB 61 LQKPGQSPKLLIYKYSNRFSGVDPDRFSGSGSTDTLTLSRYEADLVGYTCFQGTTHAPY 120
 QY 121 TFGGGTKLEIKRTAAAPSVFIPTPSDQKSGTASVVCILNNFYPRBAKQMKVDNALOSG 180
 DB 121 TFGGGTKLEIKRTAAAPSVFIPTPSDQKSGTASVVCILNNFYPRBAKQMKVDNALOSG 180
 QY 181 NSQESVTEQDSKDYSLSTLTLSKADYERKHYVACEVTHQGLSSPYTKSFNRGEC 237
 DB 181 NSQESVTEQDSKDYSLSTLTLSKADYERKHYVACEVTHQGLSSPYTKSFNRGEC 237

RESULT 2
 AAM14937

ID AAM14937 standard; protein; 238 AA.

XX AAM14937;

XX 16-JUN-1997 (first entry)

XX Murine anti-porcine VCAM 3F4 light chain.

XX Xenotransplantation; graft rejection; cell interaction; pig;

XX vascular cell adhesion molecule; VCAM; monoclonal antibody;

XX chimeric antibody; diagnosis.

XX Mus sp.

XX Key Location/Qualifiers

XX Region 43..58

XX Region 74..80

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX WPI; 1997-212855/19.
 DR N-PsDB; AAT62934.
 XX Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.

PS Disclosure; Page 52-53; 105pp; English.

CC Light chain (AAM14937) and heavy chain (AAM14938) sequences are provided
 CC for the murine anti-porcine soluble vascular cell adhesion molecule
 CC (VCAM) monoclonal antibody (Mab) 3F4. Hybridoma 3F4 was produced by
 CC standard techniques using recombinant, soluble porcine VCAM as immunogen.
 CC Chimeric antibodies can be produced by cloning Mab 3F4 and 2A2 (see also
 CC AAM14931-32) variable regions into expression plasmid pAPEX-3P modified
 CC to contain the human gamma4 constant region in place of the human gamma1
 CC C1 region. Sequences are provided for 3F4 (chimeric) human G2/G4 cDNA
 CC (AAM14939), a 3F4 human G2/G4 expression plasmid insert product
 CC (AAM14940), and 3F4 human IgG4 expression plasmid insert product
 CC (AAM14941-42). The chimeric antibodies are specific for porcine VCAM.
 CC They are useful for diagnosing human rejection of porcine xenotransplants
 CC and for improving xenotransplantation of porcine cells, tissues and
 CC organs into human recipients

CC Sequence 238 AA;

Query Match 95.4%; Score 1175.5; DB 2; Length 238;
 Best Local Similarity 95.0%; Pred. No. 1.1e-65;
 Matches 226; Conservative 6; Mismatches 5; Indels 1; Gaps 1;

QY 1 MRLPVRLVLMFWIPASSSDVMTQTPLSLPVLSDQASISCRSSQTIYHSNGNTYLEMY 60
 DB 1 MRLPVRLVLMFWIPASSSDVMTQTPLSLPVLSDQASISCRSSQTIYHSNGNTYLEMY 60
 QY 61 LQKPGQSPKLLIYKYSNRFSGVDPDRFSGSGSTDTLTLSRYEADLVGYTCFQGTTHAPY 120
 DB 61 LQKPGQSPKLLIYKYSNRFSGVDPDRFSGSGSTDTLTLSRYEADLVGYTCFQGTTHAPY 120
 QY 121 TFGGGTKLEIKRTAAAPSVFIPTPSDQKSGTASVVCILNNFYPRBAKQMKVDNALOS 179
 DB 121 TFGGGTKLEIKRTAAAPSVFIPTPSDQKSGTASVVCILNNFYPRBAKQMKVDNALOS 180
 QY 180 GNSQESVTEQDSKDYSLSTLTLSKADYERKHYVACEVTHQGLSSPYTKSFNRGEC 237
 DB 181 GNSQESVTEQDSKDYSLSTLTLSKADYERKHYVACEVTHQGLSSPYTKSFNRGEC 238

RESULT 3
 AAM14942

ID AAM14942 standard; protein; 238 AA.

XX AAM14942;

XX 16-JUN-1997 (first entry)

XX 3F4 Human IgG4 expression plasmid insert product (light chain).

XX Xenotransplantation; graft rejection; cell interaction; pig;

XX vascular cell adhesion molecule; VCAM; monoclonal antibody;

XX chimeric antibody; diagnosis.

XX Mus sp.

XX Key Location/Qualifiers

XX Region 43..58

XX Region 74..80

XX Region 113..121

XX Region 113..121

XX Region 113..121

XX Region 113..121

PA (ALEX-) ALEXION PHARM INC.
 XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matris LA;
 XX WPI, 1997-212855/19.
 DR N-PSDB; AAI62938.
 XX
 XX Antibodies binding to porcine but not human cell interaction proteins -
 PT useful to treat and assay for rejection of xenografted porcine organs,
 PT tissues or cells.
 XX
 XX Disclosure; Page 65-66; 105pp; English.
 PS
 XX Heavy chain (AAW14941) and light chain (AAW14942) sequences correspond to
 CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
 CC monoclonal antibody 3F4 (see also AAW14937-38). They are encoded by a 3F4
 CC human IgG4 expression plasmid insert (see also AAI62938). A chimeric
 CC antibody specific for porcine VCAM can be produced in transfectected host
 CC cells. It is useful for diagnosing human rejection of porcine
 CC xenotransplants and for improving xenotransplantation of porcine cells,
 CC tissues and organs into human recipients
 XX
 XX Sequence 238 AA;
 SQ
 Query Match 95.4%; Score 1175.5; DB 2; Length 238;
 Best Local Similarity 95.0%; Pred. No. 1,1e-65;
 Matches 226; Conservative 6; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSGNTYLEMY 60
 Db 1 MKLPVRLVLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSGNTYLEMY 60
 QY 61 LQKQGSFKLIIYKSNRFGSGVDPDFSSGSGTDTLTKISREADLGVYFCOGTHAPY 120
 Db 61 LQKQGSFKLIIYKSNRFGSGVDPDFSSGSGTDTLTKISREADLGVYFCOGTHAPY 120
 QY 121 TFGGTTKLEIK-TAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQS 179
 Db 121 TFGGTTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQS 180
 QY 180 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSPVTKSPFNNGEC 237
 Db 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSPVTKSPFNNGEC 238
 RESULT 4
 ABP58288
 ID ABP58288 standard; protein; 238 AA.
 XX
 XX AC ABP58288;
 XX
 DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX
 DE Humanised 10D5 antibody light chain.
 XX
 XX Monoclonal antibody; 10D5; complementarity determining region; CDR;
 KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 OS
 XX Key
 FT Peptide
 FT Peptide
 FT Peptide
 FT Region
 FT Region
 FT Region
 Location/Qualifiers
 1..19
 /label= Signal_peptide
 20..238
 /label= Mature_protein
 /note= "the mature light chain is claimed in Claim 5"
 20..132
 /note= "light chain variable region, claimed in Claim 4"
 43..58

FT /note= "CDR1"
 FT Region 74..80
 FT /note= "CDR2"
 FT Region 113..121
 FT /note= "CDR3"
 XX
 XX WO200288307-A2.
 XX
 XX PD 07-NOV-2002.
 XX
 XX 26-APR-2002; 2002WO-US011854.
 XX
 XX 30-APR-2001; 2001US-0287653P.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Hinton PR, Vasquez M;
 XX WPI; 2003-183836/18.
 DR N-PSDB; AB224638, AB224640.
 XX
 XX New humanized 10D5 antibody, useful for the manufacture of a medicament
 PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
 PT disease or cerebral amyloid angiopathy.
 XX
 XX Disclosure; Page 13; 52pp; English.
 PS
 XX The present sequence is the protein sequence of the light chain of a
 CC humanised antibody of the present invention. In the variable portion, the
 CC complementarity determining regions (CDRs) originate from murine
 CC monoclonal antibody 10D5 and the framework region originates from human
 CC germline V_K segment DPK18 and J segment Jk4. Novel humanised antibodies
 CC of the invention have CDRs from 10D5 and human framework sequences. These
 CC humanised antibodies have binding affinities (affinity and epitope
 CC location) approximately the same as those of the mouse 10D5 antibody. The
 CC invention includes antibodies, single chain antibodies, and their
 CC fragments, as well as nucleotide sequences, vectors, transformed host
 CC cells, and methods of using the humanised antibody to treat, prevent,
 CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
 CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
 CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
 CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
 CC OS field)
 XX
 XX Sequence 238 AA;
 SQ
 Query Match 94.5%; Score 1164.5; DB 6; Length 238;
 Best Local Similarity 93.7%; Pred. No. 5.2e-65;
 Matches 223; Conservative 8; Mismatches 6; Indels 1; Gaps 1;
 QY 1 MKLPVRLVLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSGNTYLEMY 60
 Db 1 MKLPVRLVLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSGNTYLEMY 60
 QY 61 LQKQGSFKLIIYKSNRFGSGVDPDFSSGSGTDTLTKISREADLGVYFCOGTHAPY 120
 Db 61 LQKQGSFKLIIYKSNRFGSGVDPDFSSGSGTDTLTKISREADLGVYFCOGTHAPY 120
 QY 121 TFGGTTKLEIK-TAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQS 179
 Db 121 TFGGTTKLEIKRTVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQMKVDNALQS 180
 QY 180 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSPVTKSPFNNGEC 237
 Db 181 GNSQSVTEQDSKDSYSLSTLTLSKADYKHKYACEVTHQGLSPVTKSPFNNGEC 238
 RESULT 5
 AAU07744
 ID AAU07744 standard; protein; 238 AA.
 XX
 XX AC AAU07744;
 XX

XX	04-DEC-2001	(first entry)	
DT			
XX			
DE	Humanised monoclonal antibody Hu266, light chain.		
XX			
KW	Monoclonal antibody; Hu266; nootropic; neuroprotective; Abeta peptide;		
KW	Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy;		
KW	gene therapy.		
XX			
OS	Mus sp.		
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	Peptide	1..19	
FT		/label= Signal_peptide	
FT	Protein	20..238	
FT		/label= Mature_Hu266_light_chain	
FT		/note= "This sequence is specifically claimed in claim 17"	
XX			
XX	WO200162801-A2.		
XX			
PD	30-AUG-2001.		
XX			
PE	26-FEB-2001; 2001WO-US006191.		
XX			
XX	24-FEB-2000; 2000US-0184601P.		
PR	08-DEC-2000; 2000US-0254465P.		
PR	08-DEC-2000; 2000US-0254498P.		
XX			
PA	(UNIM) UNIV WASHINGTON.		
PA	(EHL) LILLY & CO ELI.		
XX			
PI	Holtzman DM, Demattos R, Bales KR, Paul SM, Tsunashima N;		
PI	Vasquez M;		
XX			
XX	MP1: 2001-550087/61.		
DR	N-P8DB; AAS11981.		
XX			
XX	New humanized antibody for the treatment of Alzheimer's comprises the		
PT	inhibition and reduction of the formation of amyloid plaques.		
XX			
PS	Example 13; Fig 4; 63pp; English.		
XX			
CC	The invention relates a humanised antibody that specifically binds an		
CC	epitope contained within positions 13-28 of amyloid beta peptide, Abeta.		
CC	The antibody is useful to inhibit and reduce the formation of amyloid		
CC	plaques or the effects of toxic soluble Abeta species in humans their		
CC	fragments are used for the manufacture of a medicant. This includes the		
CC	prolonged expression of recombinant sequences of them in human tissues		
CC	for the treatment of clinical/pre-clinical Alzheimer's disease, Down's		
CC	syndrome or pre clinical cerebral amyloid angiopathy. Specifically, the		
CC	antibody is used to sequester Abeta into plasma, brain or cerebrospinal		
CC	fluid to prevent/reverse accumulation of the Abeta peptide within the		
CC	brain thereby improving cognition. The present sequence is the light		
CC	chain of a humanised monoclonal antibody, Hu266, based on the mouse		
CC	antibody 266		
XX			
XX			
SQ	Sequence 238 AA;		
Query Match	90.4%;	Score 1113.5;	DB 4; Length 238;
Best Local Similarity	89.5%;	Pred. No. 7,9e-62;	
Matches 213;	Conservative 13;	Mismatches 11;	Indels 1; Gaps 1
QY	1	MKLPLRLVITAMWIPASSSDVMTQPLSLPVSIGDQASISCRSSGQTIVHSNGNTYLEMY	60
DB	1	MKLPLRLVITAMWIPASRCVDMTQSPSLPVTLQGPASISCRSSGSLIYSDGNALHMF	60
QY	61	LQKPGQSPLILYKYNSNRFSGVDPDRSGSGSGTDFTLKISRVAEDLGYVYCFQGTTHAY	120
DB	61	LQKPGQSRPLILYKYNSNRFSGVDPDRSGSGSGTDFTLKISRVAEDVGYVYCGSGTHVM	120
QY	121	TFGGGKTLEIK-TAAAPSVFIFFPPSDQLKSGTASVVCILNNFFPREARVQMKVDNALGS	179

Db	121	TFGGATKVEIKRTYAAPSVFI	FPSPDEDLKSGTASV	CVCLINNFFYRRAAVQKVDALGS	180
Qy	180	GNQGESVTBODSKDSTYSLS	STLTISKADYERKHYACEVTH	QGLSSPYTKSPNRGEC	237
Db	181	GNQGESVTBODSKDSTYSLS	STLTISKADYERKHYACEVTH	QGLSSPYTKSPNRGEC	238
RESULT 6					
ID	ABR39842	standard; protein; 238 AA.			
XX	ABR39842;				
AC	ABR39842;				
XX	18-AUG-2003	(first entry)			
XX	Humanised anti-Abeta antibody 266 light chain.				
XX	Amyloid-beta; Abeta; antibody 266; neurotropic; neuroprotective; CDR;				
XX	immunostimulant.				
XX	Homo sapiens.				
XX	MO2003016466-A2.				
XX	27-FEB-2003.				
XX	14-AUG-2002; 2002WO-US021322.				
XX	17-AUG-2001; 2001US-0313224P.				
XX	(EHL) LILLY & CO ELI.				
PA	Jia AY, Tsurnushita N, Vaequez MJ;				
PI	WPI; 2003-278557/27.				
XX	N-PSDB; ACC47226.				
DR	New antibodies comprising a heavy chain and a light chain complementarity				
PT	determining regions from antibody 266, for treating and preventing				
PT	conditions associated with the A beta peptide, e.g. Alzheimer's disease				
PT	or Down syndrome.				
XX	Disclosure; Fig 1; 82pp; English.				
PS	The invention relates to an anti-Abeta (amyloid-beta peptide) antibody				
XX	266. The antibodies are useful for treating and preventing conditions				
CC	associated with the Abeta peptide, such as Alzheimer's disease, Down				
CC	syndrome, and cerebral amyloid angiopathy; for diagnosing diseases in				
CC	humans; for determining whether a human subject will respond to treatment				
CC	using humanised antibodies against Abeta; for treating, preventing and				
CC	reversing cognitive decline in clinical or pre-clinical Alzheimer's				
CC	disease, Down's syndrome or cerebral amyloid angiopathy; for inhibiting				
CC	formation of amyloid plaques of the effects of toxic soluble Abeta				
CC	species in humans. Treatment of the patients with antibody will inhibit				
CC	or prevent cognitive decline typically associated with disease				
CC	progression and reverses it. The present sequence represents a humanised				
CC	anti-Abeta antibody 266 light chain				
XX	Sequence 238 AA;				
Qy	Query Match	90.4%;	Score 1113.5;	DB 6;	Length 238;
Db	Beat Local Similarity	89.5%;	Pred. No. 7.9e-62;		
Db	Matches 213; Conservative 13;	Mismatches 11;	Indels 1;	Gaps 1	
Qy	1	MKLPRLLVLMFWPIAASSSDVMTGTPPLSLPISLGDQASISCRSGTIYHSNGNTLYBY	60		
Db	1	MKLPRLLVLMFWPIAASCDVMTGTPPLSLPPTLQOPASISCRSGSLIYSGDNATLHWF	60		
Qy	61	LQKPGQSKLLIYKYSNRPFGVDRFSGSGSGTDFTLKSRVBAEDLGYVYCGQGTAPY	120		
Db	61	LQKPGQSKLLIYKYSNRPFGVDRFSGSGSGTDFTLKSRVBAEDVGYVYCGQSTHVP	120		

[illegible][illegible]

Db 61 YLQKQGSPRLIIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGCVYYCSQSTHP 120
 QY 120 YTFGGGTLEIK-TAAPSVPFIFPPSDQLKSGTASVCLLNNFYPREAKVQMKVDNALQ 178
 Db 121 PAFGGGTKEIKRTVAAPSVPFIFPPSDQLKSGTASVCLLNNFYPREAKVQMKVDNALQ 180
 QY 179 SGNQSESVTEODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVYTKSFNRGEC 237
 Db 181 SGNQSESVTEODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVYTKSFNRGEC 239

RESULT 12

AA012915
 ID AAB12915 standard; protein; 239 AA.

AA012915;
 AC AAB12915;
 XX 16-NOV-2000 (first entry)
 DT 16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M light chain protein sequence SEQ ID #82.

KM Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody.

OS Synthetic.

PN JP2000154149-A.

PD 06-JUN-2000.

PF 17-SEP-1999; 99JP-00263984.

PR 18-SEP-1998; 98JP-00264598.

XX (SANY) SANKYO CO LTD.

XX WPI; 2000-454476/40.

DR N-PSDB; AAA78269.

XX Anti-human Fas humanizing antibody-containing antirheumatic agents.

PS Claim 1; Page 70-71; 109pp; Japanese.

XX The present invention relates to antirheumatic agents which comprise as
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
 CC does not include a J segment, has apoptosis inducing activity, and
 CC consists of a light and heavy chain polypeptide produced synthetically.
 CC The agents of the invention exhibit antirheumatic and immunosuppressive
 CC activity and can be used to treat autoimmune diseases, especially
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
 CC binding properties. Included in the invention are nucleotide sequences of
 CC the IgM light and heavy chains (see AAA78267-A78272) and the
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
 CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences AAA78213-
 CC A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAA78277-A78318 and AAA78335-
 CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention

XX Sequence 239 AA;

Query Match 88.6%; Score 1091; DB 3; Length 239;

Best Local Similarity 87.9%; Pred. No. 2e-60;
 Matches 210; Conservative 13; Mismatches 14; Indels 2; Gaps 2;

QY 1 MKLPVRL-LVLMFWIRASSSDVIMTQTPLSLPSVLQDQASISCRSQTIVHSNGNTYLEW 59

Db 1 MKLPVRL-LVLMFWIRASSSDVIMTQTPLSLPSVLQDQASISCRSQTIVHSNGNTYLEW 60
 QY 60 YLQKQGSPRLIIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGCVYYCSQSTHP 119
 Db 61 YLQKQGSPRLIIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGCVYYCSQSTHP 120
 QY 120 YTFGGGTLEIK-TAAPSVPFIFPPSDQLKSGTASVCLLNNFYPREAKVQMKVDNALQ 178
 Db 121 PAFGGGTKEIKRTVAAPSVPFIFPPSDQLKSGTASVCLLNNFYPREAKVQMKVDNALQ 180
 QY 179 SGNQSESVTEODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVYTKSFNRGEC 237
 Db 181 SGNQSESVTEODSKSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVYTKSFNRGEC 239

RESULT 13

AA071877
 ID AAW71877 standard; protein; 239 AA.

AA071877;
 AC AAW71877;
 XX 18-JAN-1999 (first entry)
 DT 18-JAN-1999 (first entry)

DE Anti-human Fas humanised antibody CH11 light chain VL-KF.

KM Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.

OS Homo sapiens.

OS Synthetic.

XX Key Location/Qualifiers

XX Peptide 1..20

XX Protein 21..239

XX Region 44..59

XX /label= CDR1

XX /note= "complementarity determining region 1 from CH11

XX light chain"

XX /label= CDR2

XX /note= "complementarity determining region 2 from CH11

XX light chain"

XX /label= CDR3

XX /note= "complementarity determining region 3 from CH11

XX light chain"

XX Region

XX 75..81

XX /label= CDR2

XX /note= "complementarity determining region 2 from CH11

XX light chain"

XX /label= CDR3

XX /note= "complementarity determining region 3 from CH11

XX light chain"

XX Region

XX 20-MAR-1998; 98EP-00302113.

XX 21-MAR-1997; 97JP-00067938.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S,

XX WPI; 1998-482965/42.

XX N-PSDB; AAV61360.

XX Production of anti-Fas protein humanised antibodies - for use in inducing

XX apoptosis on Fas expressing cells in the treatment of autoimmune

XX diseases, especially rheumatoid arthritis.

XX Claim 23; Page 96-97; 187pp; English.

XX This is the amino acid sequence of a humanised anti-Fas antibody CH11

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:47:53 ; Search time 21.3605 Seconds
(without alignments)
917.306 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1332
Sequence: 1 MKLPLRLVLMFWMIPASSD.....EVTHQGLSPVTKSFNRGEC 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCRTS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1043	84.7	242	1	US-08-398-613A-56 Sequence 56, Appl
2	1043	84.7	242	1	US-08-398-612A-56 Sequence 56, Appl
3	1043	84.7	242	1	US-08-398-611A-56 Sequence 56, Appl
4	1043	84.7	242	1	US-08-491-334A-56 Sequence 56, Appl
5	1043	84.7	242	2	US-09-027-449-42 Sequence 42, Appl
6	1043	84.7	242	2	US-08-804-444A-42 Sequence 42, Appl
7	1043	84.7	242	2	US-09-026-985-42 Sequence 42, Appl
8	1043	84.7	242	2	US-09-121-952A-42 Sequence 42, Appl
9	1043	84.7	242	2	US-09-234-340A-42 Sequence 42, Appl
10	1043	84.7	242	2	US-09-355-014-42 Sequence 42, Appl
11	1029	83.5	239	2	US-08-487-550-6 Sequence 6, Appl
12	1029	83.5	239	2	US-09-526-098-6 Sequence 6, Appl
13	1029	83.5	239	2	US-09-383-916-6 Sequence 6, Appl
14	1029	83.5	239	2	US-09-758-173-6 Sequence 6, Appl
15	1029	83.5	239	2	US-09-576-424-6 Sequence 6, Appl
16	1015	82.4	239	2	US-10-000-489-8 Sequence 8, Appl
17	998.5	81.0	238	2	US-09-192-545-4 Sequence 4, Appl
18	978	79.4	238	2	US-09-698-705-10 Sequence 10, Appl
19	971	78.8	218	2	US-09-698-705-12 Sequence 12, Appl
20	963	78.2	242	2	US-09-027-449-51 Sequence 51, Appl
21	963	78.2	242	2	US-08-804-444A-51 Sequence 51, Appl
22	963	78.2	242	2	US-09-026-985-51 Sequence 51, Appl
23	963	78.2	242	2	US-09-121-952A-51 Sequence 51, Appl
24	963	78.2	242	2	US-09-234-340A-51 Sequence 51, Appl
25	963	78.2	242	2	US-09-355-014-51 Sequence 51, Appl
26	957	77.7	242	2	US-09-027-449-62 Sequence 62, Appl
27	957	77.7	242	2	US-09-026-985-62 Sequence 62, Appl

28	957	77.7	242	2	US-09-121-952A-62 Sequence 62, Appl
29	957	77.7	242	2	US-09-234-340A-62 Sequence 62, Appl
30	957	77.7	242	2	US-09-355-014-62 Sequence 62, Appl
31	955	77.5	242	2	US-09-027-449-56 Sequence 56, Appl
32	955	77.5	242	2	US-08-804-444A-56 Sequence 56, Appl
33	955	77.5	242	2	US-09-026-985-56 Sequence 56, Appl
34	955	77.5	242	2	US-09-121-952A-56 Sequence 56, Appl
35	955	77.5	242	2	US-09-234-340A-56 Sequence 56, Appl
36	955	77.5	242	2	US-09-355-014-56 Sequence 56, Appl
37	954.5	77.5	240	2	US-10-630-406-8 Sequence 8, Appl
38	951.5	77.2	219	2	US-09-027-449-72 Sequence 72, Appl
39	951.5	77.2	219	2	US-09-026-985-72 Sequence 72, Appl
40	951.5	77.2	219	2	US-09-121-952A-72 Sequence 72, Appl
41	951.5	77.2	219	2	US-09-234-340A-72 Sequence 72, Appl
42	951.5	77.2	219	2	US-09-355-014-72 Sequence 72, Appl
43	938	76.1	240	2	US-09-301-593-16 Sequence 36, Appl
44	932	75.6	241	1	US-07-916-098A-56 Sequence 56, Appl
45	923.5	75.0	239	2	US-09-627-896B-22 Sequence 22, Appl

ALIGNMENTS

RESULT 1
US-08-398-613A-56
Sequence 56, Application US/08398613A
Patent No. 5677426
GENERAL INFORMATION:
APPLICANT: Fong, Sherman
APPLICANT: Hebert, Caroline Alice
APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398, 613A
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Fites, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 874P1-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-398-613A-56
Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;
QY 7 LVLVLMFWIPASS---SDVLTMTQTPLSLPLVSLGDDQASISCRSSQRTIVHNGNVTYLEWYLOK 63

Db 8 L1ASFVFSIATNAYADIVMTQPLSLPVLSDQASISCRSSQSLVHGIGNTYLWYLOK 67
Qy 64 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEOLKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
Db 128 AGTKELKRAVAAPVFIIPSPSEOLKSGTASVCLNNFYPREAKVQKVNALQSGNS 187
Qy 183 QESVTEQDSKSTYSLSTLTLSKADYEKHKYACVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEQDSKSTYSLSTLTLSKADYEKHKYACVTHQGLSPVTSFNRGEC 242

RESULT 2
US-08-398-612A-56

/ Sequence 56, Application US/08398612A
/ Patent No. 5686070
/ GENERAL INFORMATION:
/ APPLICANT: Doershuk, Claire M.
/ APPLICANT: Fong, Sherman
/ APPLICANT: Hebert, Caroline Alice
/ APPLICANT: Kim, Kyung Jin
/ APPLICANT: Leong, Steven R.
/ TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
/ TITLE OF INVENTION: Treatment of Inflammatory Disorders
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ FILING DATE: 01-MAR-1995
/ APPLICATION NUMBER: US/08/398,612A
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/398611
/ FILING DATE: 01-MAR-1995
/ APPLICATION NUMBER: 08/205864
/ FILING DATE: 03-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P0874P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-5530
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ US-08-398-612A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 L1AFMFWIPASS---SDVMTQTPSLPVLSDQASISCRSSQSLVHGIGNTYLWYLOK 63
Db 8 L1ASFVFSIATNAYADIVMTQPLSLPVLSDQASISCRSSQSLVHGIGNTYLWYLOK 67

Qy 64 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEOLKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
Db 128 AGTKELKRAVAAPVFIIPSPSEOLKSGTASVCLNNFYPREAKVQKVNALQSGNS 187
Qy 183 QESVTEQDSKSTYSLSTLTLSKADYEKHKYACVTHQGLSPVTSFNRGEC 237
Db 188 QESVTEQDSKSTYSLSTLTLSKADYEKHKYACVTHQGLSPVTSFNRGEC 242

RESULT 3
US-08-398-611A-56

/ Sequence 56, Application US/08398611A
/ Patent No. 5702946
/ GENERAL INFORMATION:
/ APPLICANT: Doershuk, Claire M.
/ APPLICANT: Fong, Sherman
/ APPLICANT: Hebert, Caroline Alice
/ APPLICANT: Kim, Kyung Jin
/ APPLICANT: Leong, Steven R.
/ TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
/ TITLE OF INVENTION: of Inflammatory Disorders
/ NUMBER OF SEQUENCES: 58
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: WinPatIn (Genentech)
/ CURRENT APPLICATION DATA:
/ FILING DATE: 01-MAR-1995
/ APPLICATION NUMBER: US/08/398,611A
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/205864
/ FILING DATE: 03-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Love, Richard B.
/ REGISTRATION NUMBER: 34,659
/ REFERENCE/DOCKET NUMBER: P0874P1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415/225-5530
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 242 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
/ US-08-398-611A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 L1AFMFWIPASS---SDVMTQTPSLPVLSDQASISCRSSQSLVHGIGNTYLWYLOK 63
Db 8 L1ASFVFSIATNAYADIVMTQPLSLPVLSDQASISCRSSQSLVHGIGNTYLWYLOK 67
Qy 64 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 123
Db 68 PQOSPFLIYKYNSNFSGVDPDRFSGSGGSDTFTLKISRVEADLGVYCFQGTAPYTFG 127
Qy 124 GGTKEIKTA-AAPSVFIIPSPDEOLKSGTASVCLNNFYPREAKVQKVNALQSGNS 182

Db 128 AGTKLELRAVAAPVFIFFPPSSBQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNS 187
Qy 183 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 237
Db 188 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 242

RESULT 4

US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-491-334A-56

Query Match 84.7%; Score 1043; DB 1; Length 242;

Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 LLIWMFWTPASS---SDVLTMTQTPLSLPSVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 63
Db 8 LIASFVESIATNAYADIVMTQTPLSLPSVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 67
Qy 64 PGQSPKLIIVKSNRFSGVDPDRFSGSGGTDTFTLKISRVEADLGVVYCFQGTAPYTFG 123
Db 68 PGQSPKLIIVKSNRFSGVDPDRFSGSGGTDTFTLKISRVEADLGVVYCFQGTAPYTFG 127
Qy 124 GGTKEIKETA-AAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNS 182
Db 128 AGTKLELRAVAAPVFIFFPPSSBQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNS 187
Qy 183 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 237

Db 188 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 242

RESULT 5

US-09-027-449-42
; Sequence 42, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-027-449-42

Query Match 84.7%; Score 1043; DB 2; Length 242;

Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

Qy 7 LLIWMFWTPASS---SDVLTMTQTPLSLPSVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 63
Db 8 LIASFVESIATNAYADIVMTQTPLSLPSVSLGDQASISCRSSQSLVHGIGNTYLMWYLOK 67
Qy 64 PGQSPKLIIVKSNRFSGVDPDRFSGSGGTDTFTLKISRVEADLGVVYCFQGTAPYTFG 123
Db 68 PGQSPKLIIVKSNRFSGVDPDRFSGSGGTDTFTLKISRVEADLGVVYCFQGTAPYTFG 127
Qy 124 GGTKEIKETA-AAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNS 182
Db 128 AGTKLELRAVAAPVFIFFPPSSBQLKSGTASVVCLLNNFYPREAKVQMKVDNALQSGNS 187
Qy 183 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 237
Db 188 QESVTEODSKDSTYSLSTLTLSKADYERKHRYACEVTHQGLSSPVTSFNRGEC 242

RESULT 6

US-08-804-444A-42
Sequence 42, Application US/0880444A
Patent No. 6117980
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania N
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,444A
FILING DATE: 21-Feb-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-804-444A-42

Query Match 84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LILVIMFWIPASS--SDVIMTQTPLSLPVSLGDQASISCRSSQTIVHNSGNTYLEMYLQK 63
DB 8 ILASMFVSIATNAVADIYMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMYLYQK 67

QY 64 PQOSPRLIYKXSNRFSGVPPDRFSGSGGTDTLTIRSRVADLGLYFCSQSTHVPFLPG 123
DB 68 PQOSPRLIYKXSNRFSGVPPDRFSGSGGTDTLTIRSRVADLGLYFCSQSTHVPFLPG 127

QY 124 GGTKEIKTA-AAPSVFIPPSDQKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
DB 128 AGTKLEIKRAVAAPVFIFFPSSQKSGTASVCLNNFYPREAKVQKVNALQSGNS 187

QY 183 QBSVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPYTKSPFNNGEC 237
DB 188 QBSVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPYTKSPFNNGEC 242

RESULT 7
US-09-026-985-42
Sequence 42, Application US/09026985
Patent No. 6133426
GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/026,985
FILING DATE: 20-Feb-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R3-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-026-985-42

Query Match 84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LILVIMFWIPASS--SDVIMTQTPLSLPVSLGDQASISCRSSQTIVHNSGNTYLEMYLQK 63
DB 8 ILASMFVSIATNAVADIYMTQTPLSLPVSLGDQASISCRSSQSLVHGIGNTYLMYLYQK 67

QY 64 PQOSPRLIYKXSNRFSGVPPDRFSGSGGTDTLTIRSRVADLGLYFCSQSTHVPFLPG 123
DB 68 PQOSPRLIYKXSNRFSGVPPDRFSGSGGTDTLTIRSRVADLGLYFCSQSTHVPFLPG 127

QY 124 GGTKEIKTA-AAPSVFIPPSDQKSGTASVCLNNFYPREAKVQKVNALQSGNS 182
DB 128 AGTKLEIKRAVAAPVFIFFPSSQKSGTASVCLNNFYPREAKVQKVNALQSGNS 187

QY 183 QBSVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPYTKSPFNNGEC 237
DB 188 QBSVTEQDSKDSYSLSTLTLSKADYERKHYACEVTHQGLSSPYTKSPFNNGEC 242

RESULT 8
US-09-121-952A-42
Sequence 42, Application US/09121952A
Patent No. 6458355
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shirokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952A
FILING DATE: 24-JUL-1998
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-121-952A-42

Query Match      84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LVLVFWIPASS---SDVLTMTQTPSLPVSIGDQASISCRSSQTIVHSGNGTYLEMYLQK 63
DB 8 LLASMFVSINATNAADIVMTQTPSLPVSIGDQASISCRSSQSI VHIGNTYLYLHWYLOK 67
QY 64 PGQSPKLIIVYKSNRFGSGVDPDRFGSGSGGTDFTLKISVNEADLGVYICFGCTAAPTFFG 123
DB 68 PGQSPKLIIVYKSNRFGSGVDPDRFGSGSGGTDFTLKISVNEADLGVYICFGCTAAPTFFG 127
QY 124 GGTLEIKETA--AASVVFPPPSDEOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 182
DB 128 AGTKLELRRAVAAPVFIFFPSSSQOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 187
QY 183 QESVTEQDSKQSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTSPFRNGEC 237
DB 188 QESVTEQDSKQSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTSPFRNGEC 242

RESULT 9
US-09-234-340A-42
Sequence 42, Application US/09234340A
Patent No. 6468532
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., HseI, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,340A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/121,952
FILING DATE: 24-JUL-1998
APPLICATION NUMBER: 60/074330
FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075467
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-234-340A-42

Query Match      84.7%; Score 1043; DB 2; Length 242;
Best Local Similarity 86.4%; Pred. No. 6.5e-86;
Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LVLVFWIPASS---SDVLTMTQTPSLPVSIGDQASISCRSSQTIVHSGNGTYLEMYLQK 63
DB 8 LLASMFVSINATNAADIVMTQTPSLPVSIGDQASISCRSSQSI VHIGNTYLYLHWYLOK 67
QY 64 PGQSPKLIIVYKSNRFGSGVDPDRFGSGSGGTDFTLKISVNEADLGVYICFGCTAAPTFFG 123
DB 68 PGQSPKLIIVYKSNRFGSGVDPDRFGSGSGGTDFTLKISVNEADLGVYICFGCTAAPTFFG 127
QY 124 GGTLEIKETA--AASVVFPPPSDEOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 182
DB 128 AGTKLELRRAVAAPVFIFFPSSSQOLKSGTASVCLNNFYPREAKVQMKVDNALQSGNS 187
QY 183 QESVTEQDSKQSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTSPFRNGEC 237
DB 188 QESVTEQDSKQSTYSLSTLTLSKADYKHKYVACEVTHQGLSSPVTSPFRNGEC 242

RESULT 10
US-09-355-014-42
Sequence 42, Application US/09355014
Patent No. 6670033
GENERAL INFORMATION:
APPLICANT: Genentech, Inc., HseI, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leon, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shatrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
```


TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPVRLI-VLMFMIIPASSSDVLTMTOTPLSLPVSLGDOASISCRSSQTIHNSNGTYLEW 59
DB 1 MSLPQALLGLLILCVPGSSGVEVMTQSPLSIPITGEPASISCRSSQSLKHSNGDTPLSW 60
QY 60 YLQKPGSPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCFQGTAP 119
DB 61 YQKRGQPPRLIYKVSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCQGTPTP 120
QY 120 YTFGGGTLEIK-TAAAPSVIFPPSDPQLKSGTASVCLNNFPYPRKAYQWKVDNALQ 178
DB 121 PTFGGGTVEIKRTVAAPSVIFPPSDPQLKSGTASVCLNNFPYPRKAYQWKVDNALQ 180
QY 179 SGNQSESTVEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGRC 237
DB 181 SGNQSESTVEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGRC 239

RESULT 13

US-09-383-916-6
Sequence 6, Application US/09383916
Patent No. 6709654

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPVRLI-VLMFMIIPASSSDVLTMTOTPLSLPVSLGDOASISCRSSQTIHNSNGTYLEW 59
DB 1 MSLPQALLGLLILCVPGSSGVEVMTQSPLSIPITGEPASISCRSSQSLKHSNGDTPLSW 60
QY 60 YLQKPGSPKLLIYKVSNRFSGVDPDRFSGSGGTDFTLKISRVEAEDGIVYYCFQGTAP 119
DB 61 YQKRGQPPRLIYKVSNRDSGVDPDRFSGSGAGTDFTLKISAVEAEDGVYFCQGTPTP 120
QY 120 YTFGGGTLEIK-TAAAPSVIFPPSDPQLKSGTASVCLNNFPYPRKAYQWKVDNALQ 178
DB 121 PTFGGGTVEIKRTVAAPSVIFPPSDPQLKSGTASVCLNNFPYPRKAYQWKVDNALQ 180
QY 179 SGNQSESTVEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGRC 237
DB 181 SGNQSESTVEDSDKSTYSLSTLTLSKADYEKHKVYACEVTHQGLSSPTKSFNRGRC 239

RESULT 14

US-09-758-173-6
Sequence 6, Application US/09758173
Patent No. 6893638

GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,173
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-758-173-6

Query Match 83.5%; Score 1029; DB 2; Length 239;
Best Local Similarity 83.3%; Pred. No. 1.2e-84;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MKLPVRLI-VLMFMIIPASSSDVLTMTOTPLSLPVSLGDOASISCRSSQTIHNSNGTYLEW 59
DB 1 MSLPQALLGLLILCVPGSSGVEVMTQSPLSIPITGEPASISCRSSQSLKHSNGDTPLSW 60

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:37:39 ; Search time 153.339 Seconds
(without alignments)
1333.818 Million cell updates/sec

Title: US-10-828-782A-18
Perfect score: 2450
Sequence: 1 MECSVMFLSLGTAVLSE.....MHKALHNYTKSLSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseqp1980s:.*
2: geneseqp1980s:.*
3: geneseqp2000s:.*
4: geneseqp2001s:.*
5: geneseqp2002s:.*
6: geneseqp2003as:.*
7: geneseqp2003bs:.*
8: geneseqp2004s:.*
9: geneseqp2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2490	100.0	462	ADU70079	ADU70079 Mouse/hum
2	2174	87.3	470	AAU74296	AAU74296 Anti-huma
3	2172.5	87.2	471	AD828427	AD828427 Human ant
4	2170.5	87.2	463	AAW14939	AAW14939 3F4 (Chim
5	2170.5	87.2	463	AAW14940	AAW14940 3F4 (Chim
6	2153	86.5	464	AEA41032	AEA41032 Human ant
7	2146	86.2	462	AD257693	AD257693 Anti-cMet
8	2145.5	86.2	446	AD751705	AD751705 Visilizum
9	2143.5	86.1	442	AD751693	AD751693 Daclizuma
10	2143.5	86.1	469	AEBA5869	AEBA5869 Human mon
11	2142.5	86.0	446	AD751703	AD751703 Visilizum
12	2142.5	86.0	446	AD751704	AD751704 Visilizum
13	2140.5	86.0	442	AD751692	AD751692 Daclizuma
14	2140.5	86.0	442	AD751691	AD751691 Daclizuma
15	2139.5	85.9	446	AD751706	AD751706 Visilizum
16	2137.5	85.8	442	AD751694	AD751694 Daclizuma
17	2137.5	85.8	446	AD751707	AD751707 Visilizum
18	2135.5	85.8	469	AEBA5877	AEBA5877 Human mon
19	2135.5	85.8	442	AD751695	AD751695 Daclizuma
20	2135.5	85.8	450	AEBA3221	AEBA3221 Anti-CTRC
21	2128	85.5	472	AAV50157	AAV50157 Chimeric
22	2127.5	85.4	461	AAW22236	AAW22236 Humanised
23	2108	84.7	445	ADK52332	ADK52332 Human ant
24	2108	84.7	462	AAW14933	AAW14933 2A2 (Chim

25	2108	84.7	462	2	AAW14934	AAW14934 2A2 (Chim
26	2107	84.6	445	8	ADK52312	ADK52312 Human ant
27	2105	84.5	445	8	ADK52384	ADK52384 Human ant
28	2103.5	84.5	450	2	AAW34505	AAW34505 Heavy Cha
29	2103.5	84.5	450	2	AAW08755	AAW08755 Human Igg
30	2103.5	84.5	450	5	AEBA31890	AEBA31890 Full leng
31	2103.5	84.5	450	8	ADK18343	ADK18343 Amino aci
32	2103	84.5	445	8	ADK52296	ADK52296 Human ant
33	2090.5	84.0	552	2	AAK30775	AAK30775 pHS2-8.0
34	2089.5	83.9	463	8	ADMA1569	ADMA1569 Anti-inte
35	2088	83.9	462	2	AD257705	AD257705 Anti-cMet
36	2088	83.9	464	8	ADU68011	ADU68011 Mouse ant
37	2087	83.8	470	8	ADM72027	ADM72027 Chimeric
38	2086	83.8	468	9	ADV92468	ADV92468 SWS-1 chi
39	2086	83.8	468	9	ADV98531	ADV98531 Novel chi
40	2086	83.8	624	9	ADV92486	ADV92486 ChSMV/Rc
41	2086	83.8	624	9	ADV98549	ADV98549 Novel chi
42	2086	83.8	639	9	ADV92488	ADV92488 ChSMV/Rc
43	2086	83.8	639	9	ADV98551	ADV98551 Novel chi
44	2085	83.7	470	5	AAE27923	AAE27923 Human C2B
45	2085	83.7	470	6	ABB82832	ABB82832 Antibody

ALIGNMENTS

RESULT 1	ADU70079	ADU70079 standard; protein; 462 AA.
ID	ADU70079	ADU70079
AC	ADU70079;	
XX		
DT	24-FEB-2005 (first entry)	
XX		
DE	Mouse/human chimeric monoclonal antibody 6B5 heavy chain, SEQ:18.	
XX		
KW	Antibody engineering; chimeric antibody; drug dependence; phenacylidine; PCP; antidiabetic; toxicity; toxicity and intoxication;	
KW	psychiatric disorder; immunoglobulin; chimeric monoclonal antibody 6B5;	
KW	ch-mabB5; heavy chain.	
OS	Mus sp.	
OS	Homo sapiens.	
OS	Chimeric.	
PN	US2004242848-A1.	
XX		
PD	02-DEC-2004.	
XX		
PF	21-APR-2004; 2004US-00828782.	
XX		
PR	21-APR-2003; 2003US-0464190P.	
XX		
PA	(OWEN/) OWENS S M.	
XX	(LACY/) LACY H M.	
XX		
FI	Owens SM, Lacy HM;	
XX		
DR	WPI, 2005-011672/01.	
XX	N-PSDB; ADU70078.	
PT	New chimeric mouse/human monoclonal antibody for treating phenacylidine	
XX	drug abuse and toxicity comprises human immunoglobulin constant domains	
XX	and immunoglobulin variable domains of murine antibody.	
PS	Claim 6; SEQ ID NO 18; 34pp; English.	
XX		
CC	The invention relates to a chimeric mouse/human monoclonal antibody named	
CC	ch-mabB5 (see ADU70077 and ADU70079) which is specific for phenacylidine	
CC	(PCP). ch-mabB5 comprises immunoglobulin constant domains of human	
CC	origin and immunoglobulin variable domains from the murine anti-PCP	
CC	monoclonal antibody 6B5. The invention also relates to DNA sequences	
CC	encoding the light and heavy chains of the chimeric antibody (ADU70076	

CC and ADU70078 respectively); to expression vectors and mammalian or plant
 CC host cells comprising either of these DNA sequences; the recombinant
 CC production of the chimeric antibody; a pharmaceutical composition
 CC comprising the chimeric antibody; and a method of treating
 CC arylcyclohexylamine drug abuse using the chimeric antibody. The chimeric
 CC antibody reverses and/or reduces the adverse effects of
 CC arylcyclohexylamine drug abuse. The chimeric antibody, compositions
 CC and toxicity of the arylcyclohexylamine class of drugs such as PCP, 1-(1-
 CC (2-chienyl) cyclohexyl) piperidine (TCP) and N-ethyl-1-
 CC phenylcyclohexylamine (PCB) or other structurally similar, psychoactive
 CC analogs. The present sequence represents the chimeric heavy chain of ch-
 CC mab585.

CC Sequence 462 AA;

Query Match 100.0%; Score 2490; DB 9; Length 462;
 Best Local Similarity 100.0%; Pred. No. 3.2e-142; Mismatches 0; Gaps 0;
 Matches 462; Conservative 0; Indels 0; Gaps 0;

QY 1 MECSQVMTFLSSTAGVLSVQLQSGPELVKPGASVKNKSCASGYGTGYIHHMKQSH 60
 DB 1 MECSQVMTFLSSTAGVLSVQLQSGPELVKPGASVKNKSCASGYGTGYIHHMKQSH 60
 QY 61 GKSLEWIGIYYPNNGNGYNGKFKGKATLVTKSSSTAYMEIRLTSSDAVYCGRSTW 120
 DB 61 GKSLEWIGIYYPNNGNGYNGKFKGKATLVTKSSSTAYMEIRLTSSDAVYCGRSTW 120
 QY 121 DDPDWMGQGTTLTVSSASTKGPSVFPPLACSRSTSTALGCIWVDYPRPVTVSWNG 180
 DB 121 DDPDWMGQGTTLTVSSASTKGPSVFPPLACSRSTSTALGCIWVDYPRPVTVSWNG 180
 QY 181 ALTSQVHTPPAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKVDKVERKCCV 240
 DB 181 ALTSQVHTPPAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKVDKVERKCCV 240
 QY 241 ECPPCPAPVAGBSVFLPPPKKQDTMISRTPEVTCVVDVSHEDPEVFNMYVVGVEVH 300
 DB 241 ECPPCPAPVAGBSVFLPPPKKQDTMISRTPEVTCVVDVSHEDPEVFNMYVVGVEVH 300
 QY 301 NAKTPREPOFSTPRVSVLTVVHODMNGKVKYKKNKLPAPTEKTSKTKGQPRE 360
 DB 301 NAKTPREPOFSTPRVSVLTVVHODMNGKVKYKKNKLPAPTEKTSKTKGQPRE 360
 QY 361 POUYTLPPREBETKQVSLTCLVKGFYPSDIAVEMESGQDENNYKTPMLDSDGSPF 420
 DB 361 POUYTLPPREBETKQVSLTCLVKGFYPSDIAVEMESGQDENNYKTPMLDSDGSPF 420
 QY 421 LYSKLTVDKSRWQGNVFSQVMEHALNHHYTKSLISLSPGK 462
 DB 421 LYSKLTVDKSRWQGNVFSQVMEHALNHHYTKSLISLSPGK 462

RESULT 2
 ID AAU74296 standard; protein; 470 AA.

AC AAU74296;

DT 12-MAR-2002 (first entry)

DB Anti-human A11M monoclonal antibody clone Uma-136, heavy chain.

XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiallergic; antitumor; neuroprotective; antihypertensive; vasotrophic;
 KW immunosuppressive; dermatological; antineoplastic; hepatocellular;
 KW activation inducible lymphocyte immunomodulatory molecule; A11M;
 KW monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;
 KW multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;
 KW allergic contact-type dermatitis; chronic inflammatory dermatosis;
 KW systemic lupus erythematosus; autoimmune disorder; inflammation;
 KW graft versus host reaction; immune rejection; intestinal immunity;
 KW ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

XX Homo sapiens.
 OS WO200187981-A2.
 PN 22-NOV-2001.
 PD 15-MAY-2001; 2001WO-JP004035.
 PF 18-MAY-2000; 2000JP-00147116.
 PR 30-MAR-2001; 2001JP-00095508.
 PA (NIBS) JAPAN TOBACCO INC.
 PI Tsuji T, Tezuka K, Hori N;
 DR MPI: 2002-075313/10.
 DR N-PSDB; AAS99472.
 XX New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation.
 PS Claim 30; Page 264-266; 300pp; English.

CC The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (A11M). (I) is useful for modulating signal
 CC transduction into a cell mediated by A11M, for modulating proliferation
 CC of A11M-expressing cells, for modulating production of a cytokine from
 CC A11M-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against A11M-expressing cells and/or immune cytotoxicity or apoptosis of
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with A11M-mediated costimulatory
 CC transduction, and for inhibiting the onset and/or advancement of the
 CC diseases. (I) is useful for suppression, prevention and/or treatment of
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC psoriasis, autoimmune or allergic disorders, inflammation, graft versus
 CC host reaction, graft versus host disease, immune rejection, disorders
 CC caused by abnormal intestinal immunity, specifically inflammatory
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
 CC neoplasia, vasculitis, and pancreatitis. (I) induces no serious
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
 CC A11M monoclonal antibody amino acid sequences of the invention

XX Sequence 470 AA;

Query Match 87.3%; Score 2174; DB 5; Length 470;
 Best Local Similarity 86.4%; Pred. No. 3.9e-123; Mismatches 31; Indels 8; Gaps 1;
 Matches 406; Conservative 25;

QY 1 MECSQVMTFLSSTAGVLSVQLQSGPELVKPGASVKNKSCASGYGTGYIHHMKQSH 60
 DB 1 MECSQVMTFLSSTAGVLSVQLQSGPELVKPGASVKNKSCASGYGTGYIHHMKQSH 60
 QY 61 GKSLEWIGIYYPNNGNGYNGKFKGKATLVTKSSSTAYMEIRLTSSDAVYCGRSTW 120
 DB 61 GKSLEWIGIYYPNNGNGYNGKFKGKATLVTKSSSTAYMEIRLTSSDAVYCGRSTW 120
 QY 121 DDPDWMGQGTTLTVSSASTKGPSVFPPLACSRSTSTALGCIWVDYPRPVTVSWNG 180
 DB 121 DDPDWMGQGTTLTVSSASTKGPSVFPPLACSRSTSTALGCIWVDYPRPVTVSWNG 180
 QY 173 VTSVNSGALTSVGVHTPPAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKVDK 232
 DB 173 VTSVNSGALTSVGVHTPPAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKVDK 232
 QY 233 TYERKCCVPCPAPVAGBSVFLPPPKKQDTMISRTPEVTCVVDVSHEDPEVFNMYVVG 292
 DB 233 TYERKCCVPCPAPVAGBSVFLPPPKKQDTMISRTPEVTCVVDVSHEDPEVFNMYVVG 292

Db 241 TVERKCCVCEPCPCAPVAGPSVFLFPPKPDITLMSRTPEVTCVVDVSHEDPEVQPN 300
 QY 293 YVDGVEVHNAKTPREBQFNSTFRVSVTLTVHODMLNGKEYCKVSNKGLPAPIEKTI 352
 Db 301 YVDGVEVHNAKTPREBQFNSTFRVSVTLTVHODMLNGKEYCKVSNKGLPAPIEKTI 360
 QY 353 KTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPM 412
 Db 361 KTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTPM 420
 QY 413 LDDSGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNYTKSLSLSPGK 462
 Db 421 LDDSGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNYTKSLSLSPGK 470

RESULT 3

AD28427 ID ADE28427 standard; protein; 471 AA.

AC ADE28427;

DT 29-JAN-2004 (first entry)

DE Human anti-CD40 antibody 21-2-1 variable region heavy chain protein.

XX anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;

KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;

KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;

XX human; variable region heavy chain; 21-2-1.

OS Homo sapiens.

XX MO2003040170-A2.

XX 15-MAY-2003.

XX 08-NOV-2002; 2002WO-US036107.

XX 09-NOV-2001; 2001US-0348980P.

XX (PRIZ) PRIZER PROD INC.

XX (ABGE-) ABGENIX INC.

XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;

XX WPI; 2003-441521/41.

XX N-PSDB; ADE28426.

XX Claim 1; SEQ ID NO 34; 177pp; English.

CC The invention relates to a novel chimeric or human monoclonal antibody or
 CC its antigen-binding portion that specifically binds to and activates
 CC human CD40. The anti-CD40 antibody of the invention demonstrates
 CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
 CC activities and may be useful for treating a hyperproliferative disorder
 CC such as cancer, viral and bacterial infection or genetic, primary or
 CC combined immunodeficiency conditions including neutropenia or HIV
 CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
 CC in a biological sample in vitro or in vivo, as well as during gene
 CC therapy procedures. The current sequence is that of the human anti-CD40
 CC antibody variable region heavy chain protein of the invention.

XX Sequence 471 AA;

Query Match 87.2%; Score 2172.5; DB 7; Length 471;
 Best Local Similarity 86.2%; Pred. No. 4.8e-123;
 Matches 406; Conservative 23; Mismatches 33; Indels 9; Gaps 1;

QY 1 MECSGMVLFILSTAGVLSSEVLOQSGBELVKGASVWMSCKASGYTGTDIYIHMKQSH 60
 Db 1 MDWTRILFLVAAATGAHSQVQLVQSGAEVKKPGASVYVSCKASGYTGTGYMHVRRQAP 60
 QY 61 GKSLIEWGYIYPNNGNGYNKQEPKFKATLTVDKSSSTAYMLRITLSDSAVYTCR 117
 Db 61 GQGLIEMWGMVINDSGGNTVYAKQFGQRYMTDTISIAYMEILNLRSDITAVYYCARQDP 120
 QY 118 -----STWDDFDWMGQGTTLTVSASTKGPSVPLAPCSRSTSESTAALGLVVDYRPE 171
 Db 121 LGYCTNGVCSYFDWVGQTLTVSSASTKGPSVPLAPCSRSTSESTAALGLVVDYRPE 180
 QY 172 PVTWSNMGALITSGVHTFPFPAVLOSGLYSLSVTVTPSSNFGTQYTCNVDHKSNTKYD 231
 Db 181 PVTWSNMGALITSGVHTFPFPAVLOSGLYSLSVTVTPSSNFGTQYTCNVDHKSNTKYD 240
 QY 232 KTVERRKCCVCEPCPCAPVAGPSVFLFPPKPDITLMSRTPEVTCVVDVSHEDPEVQPN 291
 Db 241 KTVERRKCCVCEPCPCAPVAGPSVFLFPPKPDITLMSRTPEVTCVVDVSHEDPEVQPN 300
 QY 292 WYVDGVEVHNAKTPREBQFNSTFRVSVTLTVHODMLNGKEYCKVSNKGLPAPIEKTI 351
 Db 301 WYVDGVEVHNAKTPREBQFNSTFRVSVTLTVHODMLNGKEYCKVSNKGLPAPIEKTI 360
 QY 352 SKTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 411
 Db 361 SKTKGQPREPOVYTLPPSREEMTKNOVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTTP 420
 QY 412 MLDDSGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNYTKSLSLSPGK 462
 Db 421 MLDDSGSFFLYSKLTVDKSRMOQGNVSCSVMEHALHNYTKSLSLSPGK 471

RESULT 4

AAW14939 ID AAW14939 standard; protein; 463 AA.

XX AAW14939;

XX 17-OCT-2003 (revised)

XX 16-JUN-1997 (first entry)

XX 3F4 (Chimeric) human G2/G4 chimeric antibody.

XX Xenotransplantation; graft rejection; cell interaction; pig;

KW vascular cell adhesion molecule; VCAW; monoclonal antibody;

KW chimeric antibody; diagnosis.

XX Homo; sapiens.

XX Mus sp.

XX Chimeric.

XX MO9711971-A1.

XX 03-APR-1997.

XX 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 95US-0004489P.

XX 26-SEP-1996; 96US-00004489.

XX (ALEX-) ALEXION PHARM INC.

XX Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matis LA;

XX WPI; 1997-212855/19.

XX N-PSDB; AAT62936.

XX Antibodies binding to porcine but not human cell interaction proteins -

PT useful to treat and assay for rejection of xenografted porcine organs,

PT tissues or cells.

PS Disclosure; Page 56-57; 105pp; English.

XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see
CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 87.2%; Score 2170.5; DB 2; Length 463;

Best Local Similarity 88.1%; Pred. No. 6.2e-123; Matches 408; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 MECSQVFLSLSTAGTAVSEVQLQSGPELVKPGASVKMSCKASGYGTDYYIHMMKQSH 60
DB 1 MKMSVILFLSLVTAGVSHQVQVQSGAEIARPMASVLTSCASGYTNFSYMQVVKQRP 60
QY 61 GKSLFMIGIYIPNNGNGYNGKFKGKATLTVDKSSSTAYMEIRTLTSEDSAVYYCGRTW 120
DB 61 GQGLEMIIGAIYPGDDTSTYQKFRKATLTADKSSSTAYMQLSLASBSAVYYCARRTV 120
QY 121 DD-FPYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSWNS 179
DB 121 GGYFYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSWNS 180
QY 180 GALTSGVHTFPAVLOSGGLYSLSVYTVPSNFGQTYTCNVDRHPSNTKVDTERKCC 239
DB 181 GALTSGVHTFPAVLOSGGLYSLSVYTVPSNFGQTYTCNVDRHPSNTKVDTERKCC 240
QY 240 VECPCPAPVPAVAGPSVFLFPPPKDTLMISTRPEYTCVVDVDSQSDPEVQFMYYDGYEV 299
DB 241 VECPCPAPVPAVAGPSVFLFPPPKDTLMISTRPEYTCVVDVDSQSDPEVQFMYYDGYEV 300
QY 300 HNAKTKPREBOFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETKTSKTKGQPR 359
DB 301 HNAKTKPREBOFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETKTSKTKGQPR 360
QY 360 EPQVYTLPPSRREMTKNQVSLTCLVKGYFSPDAVEMESNQGPENNYKTTTPMLDSDSGF 419
DB 361 EPQVYTLPPSRREMTKNQVSLTCLVKGYFSPDAVEMESNQGPENNYKTTTPMLDSDSGF 420
QY 420 FLYSKLTVDKSRMQGNVFSQSVMEBALHNHYTQSLSLSPGK 462
DB 421 FLYSKLTVDKSRMQGNVFSQSVMEBALHNHYTQSLSLSPGK 463

RESULT 5
AAW14940
ID AAW14940 standard; protein; 463 AA.
XX AAW14940;
AC AAW14940;
XX
DT 17-OCT-2003 (revised)
DT 16-JUN-1997 (first entry)
XX
DB 3F4 (Chimeric) human G2/G4 chimeric antibody.
XX Xenotransplantation; graft rejection; cell interaction; pig;
KW vascular cell adhesion molecule; VCAM; monoclonal antibody;
KW chimeric antibody; diagnosis.
XX
OS Homo; sapiens.
OS Mus sp.
OS Chimeric.
XX
XX MO9711971-A1.
XX
XX PD 03-APR-1997.
XX
XX PF 27-SEP-1996; 96WO-US015575.

XX 28-SEP-1995; 96US-0004489P.
PR 26-SEP-1996; 96US-00004489.
XX
XX (ALEX-) ALEXION PHARM INC.
PI Mueller JP, Evans MJ, Mueller EE, Rollins S, Rother RP, Matris LA;
DR WPI; 1997-212855/19.
DR N-PSDB; AAT62937.
XX
PT Antibodies binding to porcine but not human cell interaction proteins -
PT useful to treat and assay for rejection of xenografted porcine organs,
PT tissues or cells.
XX
PS Disclosure; Page 58-61; 1055p; English.

XX A chimeric antibody (AAW14940) comprises the C1 and hinge regions of
CC human IgG2 and the C2 and C3 regions of human IgG4 (G2/G4 Mab) and a
CC murine anti-porcine soluble vascular cell adhesion molecule (VCAM)
CC monoclonal antibody (MAb) 3F4 heavy chain variable region sequence (see
CC also AAW14938). The chimeric antibody is specific for porcine VCAM. It is
CC useful for diagnosing human rejection of porcine xenotransplants and for
CC improving xenotransplantation of porcine cells, tissues and organs into
CC human recipients. (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 463 AA;

Query Match 87.2%; Score 2170.5; DB 2; Length 463;

Best Local Similarity 88.1%; Pred. No. 6.2e-123; Matches 408; Conservative 21; Mismatches 33; Indels 1; Gaps 1;

QY 1 MECSQVFLSLSTAGTAVSEVQLQSGPELVKPGASVKMSCKASGYGTDYYIHMMKQSH 60
DB 1 MKMSVILFLSLVTAGVSHQVQVQSGAEIARPMASVLTSCASGYTNFSYMQVVKQRP 60
QY 61 GKSLFMIGIYIPNNGNGYNGKFKGKATLTVDKSSSTAYMEIRTLTSEDSAVYYCGRTW 120
DB 61 GQGLEMIIGAIYPGDDTSTYQKFRKATLTADKSSSTAYMQLSLASBSAVYYCARRTV 120
QY 121 DD-FPYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSWNS 179
DB 121 GGYFYMGQTTLTYSASTKPSVFPPLAPCSRSTSESTALGCLVKDYFPEPTVSWNS 180
QY 180 GALTSGVHTFPAVLOSGGLYSLSVYTVPSNFGQTYTCNVDRHPSNTKVDTERKCC 239
DB 181 GALTSGVHTFPAVLOSGGLYSLSVYTVPSNFGQTYTCNVDRHPSNTKVDTERKCC 240
QY 240 VECPCPAPVPAVAGPSVFLFPPPKDTLMISTRPEYTCVVDVDSQSDPEVQFMYYDGYEV 299
DB 241 VECPCPAPVPAVAGPSVFLFPPPKDTLMISTRPEYTCVVDVDSQSDPEVQFMYYDGYEV 300
QY 300 HNAKTKPREBOFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETKTSKTKGQPR 359
DB 301 HNAKTKPREBOFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETKTSKTKGQPR 360
QY 360 EPQVYTLPPSRREMTKNQVSLTCLVKGYFSPDAVEMESNQGPENNYKTTTPMLDSDSGF 419
DB 361 EPQVYTLPPSRREMTKNQVSLTCLVKGYFSPDAVEMESNQGPENNYKTTTPMLDSDSGF 420
QY 420 FLYSKLTVDKSRMQGNVFSQSVMEBALHNHYTQSLSLSPGK 462
DB 421 FLYSKLTVDKSRMQGNVFSQSVMEBALHNHYTQSLSLSPGK 463

RESULT 6
AEA41032
ID AEA41032 standard; protein; 464 AA.
XX AEA41032;
AC AEA41032;
XX
XX DT 28-JUL-2005 (first entry)
XX

DE Human anti-M-CSF antibody 1.120.1 heavy chain protein SEQ ID NO:22.
 XX monoclonal antibody; macrophage colony stimulating factor inhibition;
 XX antitumor; antiproliferative; antirheumatic; virucide; antibacterial;
 XX immunosuppressive; neuroprotective; nocotropic; cerebroprotective;
 XX vasodilator; cytoskeletal; antiaesthetic; respiratory-gen.; antimetabolic;
 XX arthritis; psoriatic arthritis; rheumatoid arthritis; gout; sepsis;
 XX septic shock; endotoxic shock; Alzheimer's disease;
 XX cerebrovascular ischemia; asthma; respiratory distress syndrome;
 XX cerebral malaria; tumor; heavy chain.
 OS Homo sapiens.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /label= signal
 FT Protein 20..464
 FT Domain /note= "human anti-M-CSF antibody 1.120.1 heavy chain"
 FT 20..139
 FT /note= variable domain
 FT 45..54
 FT Region /note= "complementarity determining region CDR1"
 FT 69..85
 FT Region /note= "complementarity determining region CDR2"
 FT 118..127
 FT Region /note= "complementarity determining region CDR3"
 FT 140..464
 FT Domain /note= constant domain
 FT
 FT GB2405873-A.
 PN 16-MAR-2005.
 PD 09-SEP-2004; 2004GB-00020044.
 PF 10-SEP-2003; 2003US-0502163P.
 PR (WARN) WARNER LAMBERT CO LLC.
 XX (ABGE-) ABGENIX INC.
 PA Bedian V, Devalaraja MN, Low JE, Mobley JL, Kellermann S;
 PI Poltz I, Haak-Frendescho M;
 PI WPI; 2005-216576/23.
 DR Novel humanized, chimeric or human monoclonal antibody e.g. 9.14.41 or
 XX 8.10.3F antibody that binds to and inhibits human macrophage colony
 PT stimulating factor, useful for producing medicament for treating
 PT rheumatoid arthritis.
 XX
 PS Claim 6; SEQ ID NO 22; 155bp; English.
 XX
 CC The invention relates to a humanized, chimeric or human monoclonal
 CC antibody (I) or its antigen-binding portion that binds specifically to
 CC and inhibits human macrophage colony stimulating factor (M-CSF). Also
 CC described: (1) a polypeptide chosen from AEA41017, AEA41019, AEA41021,
 CC AEA41033, AEA41035, AEA41037, AEA41039, AEA41041, AEA41043, AEA41045,
 CC AEA41047, AEA41049, AEA41051, AEA41053, AEA41054, AEA41056,
 CC AEA41057, AEA41058, AEA41059, AEA41060, AEA41061, AEA41062, AEA41063,
 CC AEA41064, AEA41065, AEA41066, AEA41067 and AEA41068, without a signal
 CC sequence; (2) a composition (II) comprising (I) and a carrier; (3) an
 CC isolated cell line (III) for producing (I) or its antigen-binding portion
 CC or heavy or light chain of (I) or antigen-binding portions; and (4)
 CC producing (I). (I) is useful for producing a medicament for treating a
 CC condition chosen from arthritis, psoriatic arthritis, rheumatoid
 CC arthritis, gout, traumatic arthritis, rubella arthritis and acute
 CC synovitis and other arthritic conditions, sepsis, septic shock, endotoxic
 CC shock, gram negative sepsis, toxic shock syndrome, Alzheimer's disease,
 CC stroke, neurotrauma, asthma, adult respiratory distress syndrome,
 CC cerebral malaria, tumor, and chronic pulmonary inflammatory disease,
 CC preferably rheumatoid arthritis. The present sequence represents the

CC human anti-M-CSF antibody 1.120.1 heavy chain, which is used in the
 CC exemplification of the present invention.
 XX
 XX Sequence 464 AA;
 XX
 XX Query Match 86.5%; Score 2153; DB 9; Length 464;
 XX Best Local Similarity 86.9%; Pred. No. 7.1e-122;
 XX Matches 403; Conservative 23; Mismatches 36; Indels 2; Gaps 1;
 QY 1 MECSQVMTFLISGTVLSEVQLOOSGPELVKPGASVMSCKASGTYGTDYIIHMKOSH 60
 DB 1 MEWTMSFLFLVAATAGASQVQLVQSGAEVKKPQASVAVSCASGYTTSYGIISWRQNP 60
 QY 61 GKSLEMIQYIPNNNGNGYNOKFKGKATLTVDKSSSTYAMELRTTSEDSAYVYGRSTW 120
 DB 61 GQGLEMGWISAYNGNTMYAQKLDQRYMTTDTSTTAYMLKSLRSDPTAVYTCARAY 120
 QY 121 --DDEYVWGQGTTLTVSSASATKGPSPFLAPCSRSTSESTAALGLVXDYPEPTVSN 178
 DB 121 GANFPDYWGQGTTLTVSSASATKGPSPFLAPCSRSTSESTAALGLVXDYPEPTVSN 180
 QY 179 SGALTSVHTTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYDKTVERK 238
 DB 181 SGALTSVHTTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYDKTVERK 240
 QY 239 CVECPPCAPPAVAGSVFLPPKPKDMLISRTPEVTCVVDVSHEDPEVQNMVYDVG 298
 DB 241 CVECPPCAPPAVAGSVFLPPKPKDMLISRTPEVTCVVDVSHEDPEVQNMVYDVG 300
 QY 299 VHNATKPREBQPNSTPRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGP 358
 DB 301 VHNATKPREBQPNSTPRVSVLTVVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGP 360
 QY 359 REPQYITLPPEGREETKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPMLDSQS 418
 DB 361 REPQYITLPPEGREETKQVSLTCLVKGFPYSDIAVEMESNQPENNYKTTTPMLDSQS 420
 QY 419 FFLYSKLTVDKSRMQGQNVFSCSVHBALEHHNYTOKSLSLSPGK 462
 DB 421 FFLYSKLTVDKSRMQGQNVFSCSVHBALEHHNYTOKSLSLSPGK 464
 XX
 XX RESULT 7
 XX AD257693
 XX ID AD257693 standard; protein; 462 AA.
 XX
 XX AC AD257693;
 XX
 XX DT 30-JUN-2005 (first entry)
 XX
 XX DE Anti-cMet antibody 13.3.2 heavy chain protein.
 XX
 XX antibody engineering; cytoskeletal; vulnery; vasotropic; cardiant;
 XX monoclonal antibody; heavy chain; light chain; wound healing; skin ulcer;
 XX gastrointestinal ulcer; ischemia; transplant rejection;
 XX myocardial infarction; reperfusion injury; resensitis; angioplasty;
 XX vascular disease; cancer; retinopathy; endometriosis; arthritis;
 XX Alzheimer's disease; tumor; glioblastoma; sarcoma; carcinoma; diagnosis;
 XX antibody.
 OS Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 1..19
 FT Peptide /note= "signal peptide"
 FT Misc-difference 14
 FT /note= "encoded by SCA"
 FT Protein 20..462
 FT /note= "mature antibody 13.3.2 heavy chain protein"
 FT Misc-difference 42
 FT /note= "encoded by RAG"
 FT Region 50..54
 FT /note= "complementarity determining region 1"

FT	Region	69. .85	/note= "complementarity determining region 2"
FT	Misc-difference	97	/note= "encoded by WCA"
FT	Region	118. .125	/note= "complementarity determining region 3"
XX	GB2404660-A.		
XX	09-FEB-2005.		
XX	04-AUG-2004; 2004GB-00017364.		
XX	04-AUG-2003; 2003US-0492432P.		
XX	(PRIZ) PRIZER PROD INC.		
XX	(ABGE-) ABGENIX INC.		
XX	Michaud NR, Kajiji S, Borzillo G, Bedian V, Coleman K, Green LL, Jia X;		
XX	WP1; 2005-145169/16.		
XX	N-PSDB; AD257692.		
PT	Human monoclonal antibody or antigen-binding portion that specifically binds to c-Met, useful for treating cancer by inhibiting c-Met or for promoting tissue regeneration and wound healing by activating c-Met.		
PT	Claim 5; SEQ ID NO 2; 128pp; English.		
XX	The invention relates to a human monoclonal antibody (I) or its antigen-binding portion that specifically binds to c-Met, comprises a heavy chain having a fully defined sequence (S1) of 13.3.2 heavy chain, where X2 is lysine and X4 is threonine, and a light chain having a fully defined sequence (S2) of 13.3.2 light chain, where X8 is threonine, where both chains are without a signal sequence. All the sequences are fully defined in the specification. (I) is useful for the manufacture of a medicament for treating a hyperproliferative disorder in a subject, where the antibody or its portion is a c-Met antagonist. (I) is useful for manufacture of a medicament for promoting wound healing or tissue regeneration in a subject, where the antibody, antigen-binding portion or the composition activates c-Met. (I) which has a c-Met agonist activity is useful in tissue regeneration or wound healing (skin ulcers or gastric ulcers), or treating ischemia associated with kidney transplant rejection, for attenuating toxicity associated with cyclosporin treatment after transplant surgery, for treating myocardial infarction, cardiac ischemia due to reperfusion injury, restenosis after angioplasty or vascular diseases. (I) which has a c-Met antagonist activity is useful for treating cancers of brain, lung, squamous cell, bladder, neck, liver, prostate, etc., proliferative vitreoretinopathy, proliferative diabetic retinopathy, endometriosis, and arthritis, for inhibiting plaque formation in Alzheimer's disease, inhibiting cellular mitogenic responses, or for treating tumor, glioblastoma, sarcomas, or carcinomas. (I) is useful for detecting c-Met in a biological sample in vitro or in vivo, thus useful for diagnosing c-Met-expressing tumor. (I) has selectivity for c-Met that is at least 100 times greater than their selectivity for insulin like growth factor I receptor. This sequence corresponds to the antibody 13.3.2 heavy chain used in the invention.		
XX	Sequence 462 AA;		
XX	Query Match	86.2%;	Score 2146; DB 9; Length 462;
XX	Best Local Similarity	86.8%;	Pred. No. 1.9e-121;
XX	Matches	401;	Conservative 23; Mismatches 38; Indels 0; Gaps 0
QY	1 MECSGCVMLFLSGTAGVLSREVLTQSGPELVKPGASVKNSSCRASGTYGTDIYIHMKQSH 60		
DB	1 MDMTMSILFLVAAXKGAHSQVQVYVQSGAIVKKRGAASVTKSCASAGTTFITSYGSPWVRQAP 60		
QY	61 GKSLEWIGITVPRNGANGNOKRFGKAAITLVDSKSSATYAMELRTLTSEDSAYTYGCRSTW 120		
DB	61 OGGLSEMMGVIASNSNGTYYAOKLQGVVITTTDTSTSKAYMEIRLSNSDDTAVVYCARVYA 120		

QY	121	DDFDYWGQGLTLTVSSASTKGSVPLAPCASRSTSESTALGLCVNDYPRPEPTVSWNSG	180
Db	121	DYADYWGQGLTVSSASTKGSVPLAPCASRSTSESTALGLCVNDYPRPEPTVSWNSG	180
QY	181	ALTSVHFHPFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDAHKPANTKYDKVERKCCV	240
Db	181	ALTSVHFHPFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDAHKPANTKYDKVERKCCV	240
QY	241	ECPPCPAPVPVAGPSVFLFPPPKDQTLMSIRTEPVTQVVDVSHEDBEVQPMNVYDGEVH	300
Db	241	ECPPCPAPVPVAGPSVFLFPPPKDQTLMSIRTEPVTQVVDVSHEDBEVQPMNVYDGEVH	300
QY	301	NAKTYPRERFORSTRVYVSVLTVNHQDMNGEKYCKVSNKGLPAIETKTSKTKQPRE	360
Db	301	NAKTYPRERFORSTRVYVSVLTVNHQDMNGEKYCKVSNKGLPAIETKTSKTKQPRE	360
QY	361	POVYTLPPSRREMTKNQVSLTCLVNGFYPSDIAVENESGQPENNYKTTIPMLDSQGSFF	420
Db	361	POVYTLPPSRREMTKNQVSLTCLVNGFYPSDIAVENESGQPENNYKTTIPMLDSQGSFF	420
QY	421	LYSKLTVDKSRWQGNVFSQSVMEBALHNHYTQKSLSLSPGK	462
Db	421	LYSKLTVDKSRWQGNVFSQSVMEBALHNHYTQKSLSLSPGK	462
RESULT 8			
ID	ADTS1705		
XX	ADTS1705 standard; protein; 446 AA.		
AC	ADTS1705;		
XX			
DT	13-JAN-2005 (first entry)		
DE	Visilizumab antibody gamma-2M3 heavy chain mutant M428L.		
XX			
KM	Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;		
KM	FcRn binding affinity; serum half-life; dacilizumab; fexofenadine;		
KM	visilizumab; M200; cancer; inflammatory disorder; asthma;		
KM	autoimmune disease; viral infection; cytostatic; antineoplastic;		
KM	antiasthmatic; immunosuppressive; virucide; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	Misc-difference 427		
FT	/note= "Substitution of wild-type Met to Leu"		
XX			
PN	WO2004092219-A2.		
PD	28-OCT-2004.		
XX			
XX			
PF	09-APR-2004; 2004WO-US011213.		
XX			
PR	10-APR-2003; 2003US-0462014P.		
PR	03-JUN-2003; 2003US-0475762P.		
PR	29-AUG-2003; 2003US-0495048P.		
PR	15-OCT-2003; 2003US-0068711B.		
XX			
PA	(PROT-) PROTEIN DESIGN LABS INC.		
PI	Hinton PR, Teurushita N, Tso JY, Vasquez M;		
XX			
DR	WPI; 2004-758341/74.		
XX			
PT	New modified antibodies of class IgG that have altered binding affinities		
PT	for FcRn or altered serum half-lives, useful for diagnosing or treating		
PT	for e.g. cancer, inflammation, autoimmune diseases or viral infections.		
XX			
PS	Claim 22; SEQ ID NO 138; 157bp; English.		
CC	The present invention relates to a modified human antibody of class		
CC	immunoglobulin G (IgG) where at least one amino acid residue from the		

QY 354 TKGQREPOVYTLPPSRREMTKNQVSLNCTLVKGFYPSDIAVWESNGOPENNYKTTTPML 413
 DB 361 TKGQREPOVYTLPPSRREMTKNQVSLNCTLVKGFYPSDIAVWESNGOPENNYKTTTPML 420
 QY 414 DSDGSFPLYSKLTVDKSRMVGQNVFSCSVMEHAIHNHTYOKSLSPGK 462
 DB 421 DSDGSFPLYSKLTVDKSRMVGQNVFSCSVMEHAIHNHTYOKSLSPGK 469

RESULT 11
 ADTS1703 standard; protein; 446 AA.
 ADTS1703;
 ADTS1703; (first entry)
 13-JAN-2005 (first entry)
 Visilizumab antibody gamma-2M3 heavy chain mutant T250D.
 Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;
 FcRn binding affinity; serum half-life; dacilizumab; fontolizumab;
 visilizumab; M200; cancer; inflammatory disorder; asthma;
 autoimmune disease; viral infection; cytostatic; antiinflammatory;
 antitachymatic; immunosuppressive; virucide; mutant; mutein.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers
 Misc-difference 249
 FT note= "Substitution of wild-type Thr to Asp"
 XX WO2004092219-A2.
 PD 28-OCT-2004.
 XX 09-APR-2004; 2004WO-US011213.
 PF 10-APR-2003; 2003US-0462014P.
 PR 03-JUN-2003; 2003US-0475762P.
 PR 29-AUG-2003; 2003US-0499048P.
 PR 15-OCT-2003; 2003US-00687118.
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA Hinton PR, Teurushita N, Tso JY, Vasquez M;
 XX WPI: 2004-758341/74.
 DR New modified antibodies of class IgG that have altered binding affinities
 PT for FcRn or altered serum half-lives, useful for diagnosing or treating
 PT for e.g. cancer, inflammation, autoimmune diseases or viral infections.
 XX
 PS Claim 22; SEQ ID NO 136; 157bp; English.
 CC The present invention relates to a modified human antibody of class
 CC immunoglobulin G (IgG) where at least one amino acid residue from the
 CC heavy chain constant (CH) region selected from amino acid residues 250,
 CC 314 and 428 is different from that present in an unmodified class IgG
 CC antibody, and where the FcRn binding affinity and/or serum half-life of
 CC the modified antibody is altered relative to that of the unmodified
 CC antibody. The numbering of the residues in the heavy chain is that of the
 CC EU index. Also disclosed are methods of modifying an antibody of class
 CC IgG and producing the modified antibody cited, and a pharmaceutical
 CC composition comprising the above modified immunoglobulins, proteins and
 CC other bioactive molecules having altered half-lives. The unmodified or
 CC naturally occurring class IgG antibody is selected from dacilizumab,
 CC fontolizumab, visilizumab and M200. The amino acid residue 250 from the
 CC heavy chain constant region is glutamic acid or glutamine, or the amino
 CC acid residue 428 from the heavy chain constant region is phenylalanine or
 CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
 CC constant region is glutamic acid and the amino acid residue 428 from the

CC heavy chain constant region is phenylalanine, or the amino acid residue
 CC 250 from the heavy chain constant region is glutamine and the amino acid
 CC residue 428 from the heavy chain constant region is phenylalanine, or the
 CC amino acid residue 250 from the heavy chain constant region is glutamine
 CC and the amino acid residue 428 from the heavy chain constant region is
 CC leucine. The modified therapeutic antibody of class IgG has an in vivo
 CC elimination half-life of at least 1.3-fold longer than that of the
 CC corresponding unmodified class IgG antibody. The composition and methods
 CC of the invention are useful for various diagnostic and therapeutic
 CC purposes, especially in the treatment of cancer, inflammatory disorders
 CC (e.g. asthma), autoimmune diseases or viral infections. The present
 CC sequence represents a mutated region of a humanised antibody. Note: The
 CC position of the mutation is numbered according to the EU index.
 XX
 SQ Sequence 446 AA;
 Query Match 86.0%; Score 2142.5; DB 8; Length 446;
 Best Local Similarity 89.7%; Pred. No. 2.9e-121;
 Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;
 QY 20 EYVLOQSGPELVKPKASVYKMSCKASGYGTDYIHMMQSHQSLIEWIGYIPNNNGNGY 79
 DB 1 QVQLVQSGAEYKPKASVYKMSCKASGYFTSTYTHMVAQAPQGISMNGYINPRSGYTHY 60
 QY 80 NQKFKGKATLLTVDKSSSTAYNELRTLSEDSAVYVYCGRSTWDDFD--YMGQGITLVYSS 136
 DB 61 NQKFKGKATLLTVDKSSSTAYNELRTLSEDSAVYVYCGRSTWDDFD--YMGQGITLVYSS 120
 QY 137 ASTKGPVFPPLAPGCRSTSESTALGCLVKDYFPEPVTVSNAGLTSGVHTFPVAVLQSS 196
 DB 121 ASTKGPVFPPLAPGCRSTSESTALGCLVKDYFPEPVTVSNAGLTSGVHTFPVAVLQSS 180
 QY 197 GLYSLSVTVTPSSVFGQYTCNDVHKPSNKKVDTYERKCCVCPCPAPVAVGSPVY 256
 DB 181 GLYSLSVTVTPSSVFGQYTCNDVHKPSNKKVDTYERKCCVCPCPAPVAVGSPVY 240
 QY 257 LPPPKKDTLMISRTPEYTCVVDVSHEDPEVQFMVYDGVENHAKTKPREEOFNSTFR 316
 DB 241 LPPPKKDTLMISRTPEYTCVVDVSHEDPEVQFMVYDGVENHAKTKPREEOFNSTFR 300
 QY 317 VVSVLTVVHQMNLNGKEYKCKVSNKGLPAPIEKTSKTKGQREPOVYTLPPSRREMTKN 376
 DB 301 VVSVLTVVHQMNLNGKEYKCKVSNKGLPAPIEKTSKTKGQREPOVYTLPPSRREMTKN 360
 QY 377 QVSLTCLVKGFPSPDIAVWESNGOPENNYKTTTPMLDSDGFYLSKLTVDKSRMVGQGN 436
 DB 361 QVSLTCLVKGFPSPDIAVWESNGOPENNYKTTTPMLDSDGFYLSKLTVDKSRMVGQGN 420
 QY 437 VFSCSVMEHAIHNHTYOKSLSPGK 462
 DB 421 VFSCSVMEHAIHNHTYOKSLSPGK 469

RESULT 12
 ADTS1704 standard; protein; 446 AA.
 ADTS1704;
 ADTS1704; (first entry)
 13-JAN-2005 (first entry)
 Visilizumab antibody gamma-2M3 heavy chain mutant T250D.
 Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;
 FcRn binding affinity; serum half-life; dacilizumab; fontolizumab;
 visilizumab; M200; cancer; inflammatory disorder; asthma;
 autoimmune disease; viral infection; cytostatic; antiinflammatory;
 antitachymatic; immunosuppressive; virucide; mutant; mutein.
 Homo sapiens.
 Synthetic.
 Key Location/Qualifiers

```

FT Misc-difference 249 /note= "Substitution of wild-type Thr to Gln"
FT
FT
PN WO2004092219-A2.
XX
XX 28-OCT-2004.
PD
XX 09-APR-2004; 2004MO-US011213.
PF
XX 10-APR-2003; 2003US-0462014P.
XX 03-JUN-2003; 2003US-0475762P.
XX 29-AUG-2003; 2003US-0499048P.
XX 15-OCT-2003; 2003US-00687118.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Hinton PR, Teurushita N, Tso JY, Vasquez M;
XX
XX MPI; 2004-758341/74.
XX
XX New modified antibodies of class IgG that have altered binding affinities
XX for FcRn or altered serum half-lives, useful for diagnosing or treating
XX for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX
XX Claim 22; SEQ ID NO 137; 157pp; English.
XX
XX The present invention relates to a modified human antibody of class
XX immunoglobulin G (IgG) where at least one amino acid residue from the
XX heavy chain constant (CH) region selected from amino acid residues 250,
XX 314 and 428 is different from that present in an unmodified class IgG
XX antibody, and where the FcRn binding affinity and/or serum half-life of
XX the modified antibody is altered relative to that of the unmodified
XX antibody. The numbering of the residues in the heavy chain is that of the
XX EU index. Also disclosed are methods of modifying an antibody of class
XX IgG and producing the modified antibody cited, and a pharmaceutical
XX composition comprising the above modified immunoglobulin, proteins and
XX other bioactive molecules having altered half-lives. The unmodified or
XX naturally occurring class IgG antibody is selected from dactlizumab,
XX fontolizumab, visilizumab and M200. The amino acid residue 250 from the
XX heavy chain constant region is glutamic acid or glutamine, or the amino
XX acid residue 428 from the heavy chain constant region is phenylalanine or
XX leucine. Alternatively, the amino acid residue 250 from the heavy chain
XX constant region is glutamic acid and the amino acid residue 428 from the
XX heavy chain constant region is phenylalanine, or the amino acid residue
XX 250 from the heavy chain constant region is glutamine and the amino acid
XX residue 428 from the heavy chain constant region is phenylalanine, or the
XX amino acid residue 250 from the heavy chain constant region is glutamine
XX and the amino acid residue 428 from the heavy chain constant region is
XX leucine. The modified therapeutic antibody of class IgG has an in vivo
XX elimination half-life of at least 1.3-fold longer than that of the
XX corresponding unmodified class IgG antibody. The composition and methods
XX of the invention are useful for various diagnostic and therapeutic
XX purposes, especially in the treatment of cancer, inflammatory disorders
XX (e.g. asthma), autoimmune diseases or viral infections. The present
XX sequence represents a mutated region of a humanised antibody. Note: The
XX position of the mutation is numbered according to the EU index.
XX
XX Sequence 446 AA;
XX
Query Match 86.0%; Score 2142.5; DB 8; Length 446;
Best Local Similarity 89.7%; Pred. No. 2.9e-121;
Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;
XX
OY 20 EVOLQSGPELVKPGASVSKSCASGYTGDIYIHMKSHGKSLKEMIGIYPPNGANGY 79
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 QVQLVQSGAEVKKRQASVNVSCASGYTFISYTHMVRQAPOGGLGEMGYNRSQYTH 60
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 80 NQKFKGKATLTVDKSSSTAYMEIRLTTSDDSAVYYGRSTWDDFD--YWGQGTTLTVSS 136
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 NQDLKQKATLTLDKSKASTAYMEIRSEDTAVYYCARSAAYDYDGFAYWGQGTTLTVSS 120
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:
OY 137 ASKTKGSVPPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVTHFPAVLQSS 196
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
XX :|||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 121 ASKTKGSVPPLAPCSRSTSESTALGCLVKDYFPEPVTVSWNSGALTSGVTHFPAVLQSS 180
OY 197 GLYSLSVYVTPSSNFGQTQYTCNVDHKPSNTKVDKTVERRKCCVCEPCPPAPVAGPSVF 256
DB 181 GLYSLSVYVTPSSNFGQTQYTCNVDHKPSNTKVDKTVERRKCCVCEPCPPAPVAGPSVF 240
OY 257 LPPPKKDTLMISRPEEYTCVVVDVSHEDPEVFQFWYFDGVVHNAKTKPRREQFNSTR 316
DB 241 LPPPKKDTLMISRPEEYTCVVVDVSHEDPEVFQFWYFDGVVHNAKTKPRREQFNSTR 300
OY 317 VVSVLTAVHODPLNCKEYKCKVSNKGLPAPIEKTIKTKGQPRPEQVYTLPPSRREMTKN 376
DB 301 VVSVLTAVHODPLNCKEYKCKVSNKGLPAPIEKTIKTKGQPRPEQVYTLPPSRREMTKN 360
OY 377 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPMLDSGSFFLYSKLTVDKSRMQQGN 436
DB 361 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPMLDSGSFFLYSKLTVDKSRMQQGN 420
OY 437 VPSGCVMEHIALHNYTOKSLISPSRK 462
DB 421 VPSGCVMEHIALHNYTOKSLISPSRK 446
XX
XX RESULT 13
XX ADTS1692
XX ID ADTS1692 standard; protein; 442 AA.
XX
XX AC ADTS1692;
XX
XX DT 13-JAN-2005 (first entry)
XX
XX DE Dactlizumab antibody gamma-2M3 heavy chain mutant T250Q.
XX
XX KW Humanised; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;
XX FcRn binding affinity; serum half-life; dactlizumab; fontolizumab;
XX visilizumab; M200; cancer; inflammatory disorder; asthma;
XX autoimmune disease; viral infection; cytostatic; antiinflammatory;
XX antitasthmatic; immunosuppressive; vitricide; mutant; mutcin.
XX
XX OS Homo sapiens.
XX
XX SS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 245 /note= "Substitution of wild-type Thr to Gln"
XX
XX PN WO2004092219-A2.
XX
XX PD 28-OCT-2004.
XX
XX PF 09-APR-2004; 2004MO-US011213.
XX
XX PR 10-APR-2003; 2003US-0462014P.
XX 03-JUN-2003; 2003US-0475762P.
XX 29-AUG-2003; 2003US-0499048P.
XX 15-OCT-2003; 2003US-00687118.
XX
XX (PROT-) PROTEIN DESIGN LABS INC.
XX
XX Hinton PR, Teurushita N, Tso JY, Vasquez M;
XX
XX MPI; 2004-758341/74.
XX
XX New modified antibodies of class IgG that have altered binding affinities
XX for FcRn or altered serum half-lives, useful for diagnosing or treating
XX for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX
XX Claim 16; SEQ ID NO 125; 157pp; English.
XX
XX The present invention relates to a modified human antibody of class
XX immunoglobulin G (IgG) where at least one amino acid residue from the
XX heavy chain constant (CH) region selected from amino acid residues 250,
XX 314 and 428 is different from that present in an unmodified class IgG

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antibody, and where the Fc γ n binding affinity and/or serum half-life of the modified antibody is altered relative to that of the unmodified antibody. The numbering of the residues in the heavy chain is that of the EU index. Also disclosed are methods of modifying an antibody of class Igg and producing the modified antibody cited, and a pharmaceutical composition comprising the above modified immunoglobulin, proteins and other bioactive molecules having altered half-lives. The unmodified or naturally occurring class Igg antibody is selected from daclizumab, fortilizumab, visilizumab and M200. The amino acid residue 250 from the heavy chain constant region is glutamic acid or glutamine, or the amino acid residue 428 from the heavy chain constant region is phenylalanine or leucine. Alternatively, the amino acid residue 250 from the heavy chain constant region is glutamic acid and the amino acid residue 428 from the heavy chain constant region is leucine. The modified therapeutic antibody of class Igg has an in vivo elimination half-life of at least 1.3-fold longer than that of the corresponding unmodified class Igg antibody. The composition and methods of the invention are useful for various diagnostic and therapeutic purposes, especially in the treatment of cancer, inflammatory disorders (e.g. asthma), autoimmune diseases or viral infections. The present sequence represents a mutated region of a humanised antibody. Note: The position of the mutation is numbered according to the EU index.

Sequence 442 AA;

Query Match 86.0%; Score 2140.5; DB 8; Length 442;
Best Local Similarity 90.1%; Pred. No. 3.8e-121;
Matches 399; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 20 EVQLQSGPELVKPKASVYKMSCKASGYTGTYYIMMKQSHGKSLKMIQYIPNNNGNGY 79
DB 1 QVQLVQSAEYKPKSSVYKMSCKAGYFTSYRMHMTVQAPQGLMIQYINPSTGYEY 60
QY 80 NQKFKGKATLVTVDSSTAYMELRTLSEDSAVVYCGRSTMDPPYMGQGLTVTSSAST 139
DB 61 NQKFKGKATLVTVDSSTAYMELSLRSEBDNAVYICANG-GGVFYMGQGLTVTSSAST 119
QY 140 KGPVFPPLAPCSRSSTSESTAAIGCLVKDYFPEPVTVSNMNGALTSVHTFPRAVLQSSGLY 199
DB 120 KGPVFPPLAPCSRSSTSESTAAIGCLVKDYFPEPVTVSNMNGALTSVHTFPRAVLQSSGLY 179
QY 200 SLSSVTVTPSSNFGTQYTCNVDRHPSNTKVDKTVERRKCCVCEPCPAPPAVAGPSVFLFP 259
DB 180 SLSSVTVTPSSNFGTQYTCNVDRHPSNTKVDKTVERRKCCVCEPCPAPPAVAGPSVFLFP 239
QY 260 PKPDTLMISRPEVTVVNVSHEDPVOFPMYVDGVEVNAKTKPREBOGNSFFRVYS 319
DB 240 PKPDTLMISRPEVTVVNVSHEDPVOFPMYVDGVEVNAKTKPREBOGNSFFRVYS 299
QY 320 VLTAVHQMNLNGKEKCKVSNKGLPAPIEKTSKTKGQPREPOVYTLPPSRREMTKNQVS 379
DB 300 VLTAVHQMNLNGKEKCKVSNKGLPAPIEKTSKTKGQPREPOVYTLPPSRREMTKNQVS 359
QY 360 LITCLVKGFPYSDIAVEMESNGQPENNYKTPPMDLSDSFFLYSLTLTVDKSRMOQGNVFS 439
DB 360 LITCLVKGFPYSDIAVEMESNGQPENNYKTPPMDLSDSFFLYSLTLTVDKSRMOQGNVFS 419
QY 440 CSVMHEALHNHYTKQSLSLSPCK 462
DB 420 CSVMHEALHNHYTKQSLSLSPCK 442

RESURF 14
ADT51691
ID ADT51691 standard; protein; 442 AA.
AC ADT51691;
XX ADT51691;
DT 13-JAN-2005 (first entry)

XX Daclizumab antibody gamma-2M3 heavy chain mutant T250D.
DE Humanised; antibody; immunoglobulin G; Igg; gamma-2M3 heavy chain;
XX Fc γ n binding affinity; serum half-life; daclizumab; fortilizumab;
KW visilizumab; M200; cancer; inflammatory disorder; asthma;
KW autoimmune disease; viral infection; cytotoxic; antiinflammatory;
XX antiaesthetic; immunosuppressive; virucide; mutant; mutein.
OS Homo sapiens.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 245 /note= "Substitution of wild-type Thr to Asp"
FT W02004092219-A2.
XX 28-OCT-2004.
PD 09-APR-2004; 2004WO-US011213.
XX 10-APR-2003; 2003US-0462014P.
XX 03-JUN-2003; 2003US-045762P.
XX 29-AUG-2003; 2003US-0499048P.
XX 15-OCT-2003; 2003US-00687118.
XX (PROT-) PROTEIN DESIGN LABS INC.
XX Hinton PR, Teurushita N, Tso JY, Vazquez M;
PI WPI, 2004-758341/74.
XX New modified antibodies of class Igg that have altered binding affinities
XX for Fc γ n or altered serum half-lives, useful for diagnosing or treating
XX for e.g. cancer, inflammation, autoimmune diseases or viral infections.
XX Claim 16; SEQ ID NO 124; 157P; English.
PS The present invention relates to a modified human antibody of class
CC immunoglobulin G (Igg) where at least one amino acid residue from the
CC heavy chain constant (CH) region selected from amino acid residues 250,
CC 314 and 428 is different from that present in an unmodified class Igg
CC antibody, and where the Fc γ n binding affinity and/or serum half-life of
CC the modified antibody is altered relative to that of the unmodified
CC antibody. The numbering of the residues in the heavy chain is that of the
CC EU index. Also disclosed are methods of modifying an antibody of class
CC Igg and producing the modified antibody cited, and a pharmaceutical
CC composition comprising the above modified immunoglobulin, proteins and
CC other bioactive molecules having altered half-lives. The unmodified or
CC naturally occurring class Igg antibody is selected from daclizumab,
CC fortilizumab, visilizumab and M200. The amino acid residue 250 from the
CC heavy chain constant region is glutamic acid or glutamine, or the amino
CC acid residue 428 from the heavy chain constant region is phenylalanine or
CC leucine. Alternatively, the amino acid residue 250 from the heavy chain
CC constant region is glutamic acid and the amino acid residue 428 from the
CC heavy chain constant region is phenylalanine, or the amino acid residue
CC 250 from the heavy chain constant region is leucine and the amino acid
CC residue 428 from the heavy chain constant region is phenylalanine, or the
CC amino acid residue 250 from the heavy chain constant region is glutamine
CC and the amino acid residue 428 from the heavy chain constant region is
CC leucine. The modified therapeutic antibody of class Igg has an in vivo
CC elimination half-life of at least 1.3-fold longer than that of the
CC corresponding unmodified class Igg antibody. The composition and methods
CC of the invention are useful for various diagnostic and therapeutic
CC purposes, especially in the treatment of cancer, inflammatory disorders
CC (e.g. asthma), autoimmune diseases or viral infections. The present
CC sequence represents a mutated region of a humanised antibody. Note: The
CC position of the mutation is numbered according to the EU index.
XX Sequence 442 AA;

Query Match 86.0%; Score 2140.5; DB 8; Length 442;

Seq ID	Seq	Location/Qualifiers
QY	20 EVQLQQSGPELVKPAASVYMAKCAKSGYGTDTYYIHMKKSHGKSLSEIIGIYIPNNKNGCY	79
Db	1 QVQLVQSGAEVKKPKQSSVKVSCAKAGYFTSYRMHMHVRQAPQCGLEMIIGINPSIGYTEY	60
QY	80 NQKPFGRKTLTYDKSSSTAYMELRFLTSHDASVYYCGRSTMDDPFYWGQGTLLTVSSAST	139
Db	61 NQKPFGRKTLTYDKSSSTAYMELRFLTSHDASVYYCGRSTMDDPFYWGQGTLLTVSSAST	119
QY	140 KGPSVFPLAPCSRSTSESTAALGCLVKDOYFFPEPTVYSNMGALTSGVHTFPAVLQSSGLY	199
Db	120 KGPSVFPLAPCSRSTSESTAALGCLVKDOYFFPEPTVYSNMGALTSGVHTFPAVLQSSGLY	179
QY	200 SLSSVTVTPSSNFGTQYTYTCNVDRKPSNTKVDKTYERKCCVCEPCPCPAPPAVGPVFLFP	259
Db	180 SLSSVTVTPSSNFGTQYTYTCNVDRKPSNTKVDKTYERKCCVCEPCPCPAPPAVGPVFLFP	239
QY	260 PKPKDTLMISRPPELTCCVVDVSHEDPEQLQFWNYVDGVGVNNAKTKPREQKNSITRRVYS	319
Db	240 PKPKDTLMISRPPELTCCVVDVSHEDPEQLQFWNYVDGVGVNNAKTKPREQKNSITRRVYS	299
QY	320 VLTAVHQQMLNGKEKCKVSNNGKLPAPIEKTISKTKGQREPOVYTLPPSRREMTKNQVS	379
Db	300 VLTAVHQQMLNGKEKCKVSNNGKLPAPIEKTISKTKGQREPOVYTLPPSRREMTKNQVS	359
QY	380 LTCLVKGFPSPDIAVEMESNGCPENNYKTPPMLDSDGSFFLYSKLTVDKSRMQGNVS	439
Db	360 LTCLVKGFPSPDIAVEMESNGCPENNYKTPPMLDSDGSFFLYSKLTVDKSRMQGNVS	419
QY	440 CSVMHEALHNHTYOKSLSLSPGK 462	
Db	420 CSVMHEALHNHTYOKSLSLSPGK 442	
RESULT 15		
ID	ADT51706 standard; protein; 446 AA.	
AD	ADT51706;	
DT	13-JAN-2005 (first entry)	
DE	Visilizumab antibody gamma-2M3 heavy chain mutant T250Q/M428L.	
KW	Humanized; antibody; immunoglobulin G; IgG; gamma-2M3 heavy chain;	
KW	FcRn binding affinity; serum half-life; dectilzumab; fortozilzumab;	
KW	visilizumab; M200; cancer; inflammatory disorder; asthma;	
KW	autoimmune disease; viral infection; cytostatic; antiinflammatory;	
KW	antiasthmatic; immunosuppressive; vitricide; mutant; mutein.	
OS	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Misc-difference 249	/note= "Substitution of wild-type Thr to Gln"
FT	Misc-difference 427	/note= "Substitution of wild-type Met to Leu"
FN	WO2004092219-A2.	
PD	28-OCT-2004.	
PR	09-APR-2004; 2004WO-US011213.	
PR	10-APR-2003; 2003US-0462014P.	
PR	03-JUN-2003; 2003US-0475762P.	
PR	29-AUG-2003; 2003US-0499048P.	
PR	15-OCT-2003; 2003US-0068711B.	
PA	(PROT-) PROTEIN DESIGN LABS INC.	

[illegible]

Db	361	QVSLTCLVKGFPSPDIAVEMESNGQPENNNYKTPPMLDSDGSFPLYSKLTVDKSRWQGN	420
Qy	437	VFSCSVMEALHNHYTKSLSPGK	462
Db	421	VFSCSVLHEALHNHYTKSLSPGK	446

Search completed: January 24, 2006, 18:52:20
Job time : 155.339 secs

This page blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2006, 18:57:25 ; Search time 11.5279 Seconds
(without alignments)
208.348 Million cell updates/sec

Title: US-10-828-782a-16

Perfect score: 1232
Sequence: 1 MKLPVRLVLMFWIPASSD.....EVTHQGLSSPVTKSFNRGEC 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/ECT_NEM_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037	84.2	239	US-11-086-289-12	Sequence 12, Appl
2	1029	83.5	239	US-11-139-499-6	Sequence 6, Appl
3	980.5	79.6	219	US-11-080-587-8	Sequence 8, Appl
4	951	77.2	238	US-11-158-505-1	Sequence 1, Appl
5	951	77.2	238	US-11-158-505-3	Sequence 3, Appl
6	951	77.2	238	US-11-158-505-25	Sequence 25, Appl
7	951	77.2	238	US-11-158-505-27	Sequence 27, Appl
8	941	76.4	238	US-11-158-505-9	Sequence 9, Appl
9	941	76.4	238	US-11-158-505-11	Sequence 11, Appl
10	941	76.4	238	US-11-158-505-17	Sequence 17, Appl
11	941	76.4	238	US-11-158-505-19	Sequence 19, Appl
12	941	76.4	238	US-11-158-505-74	Sequence 15, Appl
13	919	74.6	233	US-11-128-900-15	Sequence 14, Appl
14	919	74.6	233	US-11-128-900-67	Sequence 67, Appl
15	916	74.4	235	US-11-128-900-14	Sequence 65, Appl
16	916	74.4	235	US-11-128-900-65	Sequence 69, Appl
17	915.5	74.3	234	US-11-128-900-17	Sequence 69, Appl
18	915.5	74.3	234	US-11-128-900-69	Sequence 69, Appl
19	912	74.0	218	US-11-158-505-4	Sequence 28, Appl
20	912	74.0	218	US-11-158-505-28	Sequence 29, Appl
21	909.5	73.8	236	US-11-096-046-25	Sequence 20, Appl
22	904.5	73.4	236	US-11-086-289-20	Sequence 12, Appl
23	902	73.2	218	US-11-158-505-12	Sequence 20, Appl
24	902	73.2	218	US-11-158-505-20	Sequence 8, Appl
25	901.5	73.2	236	US-11-086-289-8	

26	898.5	72.9	236	US-11-144-248-48	Sequence 48, Appl
27	898.5	72.9	236	US-11-144-222-48	Sequence 48, Appl
28	898	72.9	235	US-11-086-289-16	Sequence 16, Appl
29	892	72.4	218	US-11-004-590-229	Sequence 229, App
30	890.5	72.3	236	US-11-144-248-52	Sequence 52, Appl
31	890.5	72.3	236	US-11-144-222-52	Sequence 4, Appl
32	888.5	72.1	236	US-11-086-289-4	Sequence 804, Appl
33	887.5	72.0	384	US-11-000-463-804	Sequence 805, App
34	887.5	72.0	384	US-11-000-463-805	Sequence 806, App
35	887.5	72.0	384	US-11-000-463-806	Sequence 807, App
36	887.5	72.0	384	US-11-000-463-807	Sequence 335, App
37	887	72.0	363	US-11-000-463-335	Sequence 71, Appl
38	882	71.6	214	US-11-128-900-71	Sequence 47, Appl
39	880	71.4	218	US-11-084-554-11	Sequence 47, Appl
40	878.5	71.3	236	US-11-144-222-47	Sequence 47, Appl
41	878.5	71.3	236	US-11-144-222-47	Sequence 129, App
42	878	71.3	214	US-11-102-621-129	Sequence 11, Appl
43	877	71.2	214	US-11-025-712-11	Sequence 51, Appl
44	876.5	71.1	236	US-11-144-248-51	Sequence 51, Appl
45	876.5	71.1	236	US-11-144-222-51	Sequence 51, Appl

ALIGNMENTS

```

RESULT 1
US-11-086-289-12
; Sequence 12, Application US/11086289
; Publication No. US2006002929a1
; GENERAL INFORMATION:
; APPLICANT: KHARE, SANJAY D.
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES
; FILE REFERENCE: 06843.0094-00000
; CURRENT APPLICATION NUMBER: US/11/086.289
; PRIOR FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/555,396
; PRIOR FILING DATE: 2004-03-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-086-289-12

Query Match      84.2%; Score 1037; DB 7; Length 239;
Best Local Similarity 83.7%; Pred. No. 7.6e-63;
Matches 200; Conservative 16; Mismatches 21; Indels 2; Gaps 2;

QY      1 MKLPVRLVLMFWIPASSDVLMTQTPLSPVSLGDQASISCRSSQTIYHNSGNTYLEM 59
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      1 MRLAQLGLMLWVPGSGDVIWMTQPLSPVTLGPASISCRSSQSLVHSDGNTYLSW 60
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 YLQKQKSPKLLIYKVSRRPFGSGSGDTFTLKISRVKAEADGVVYCFQGTAP 119
      60 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      61 LQKRPQPLIYKFKRFGVDRFGSGAGDTFTLKISRVKAEADGVVYCFQGTAP 120
      61 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 YTFGGTLEIK-TAAPSVEIFPPSDQLKSGTAVVCLNNFYPRKAYQWKNALQ 178
      120 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      121 LTFGGTVDIKRTVAAPSVEIFPPSDQLKSGTAVVCLNNFYPRKAYQWKNALQ 180
      121 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      179 SGNQSESTEDSKDSTYLSSTLTLSKADYBEKAKVYACEVTHQGLSSPVTKSFNRGEC 237
      179 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      181 SGNQSESTEDSKDSTYLSSTLTLSKADYBEKAKVYACEVTHQGLSSPVTKSFNRGEC 239
      181 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 2
US-11-139-499-6
; Sequence 6, Application US/11139499
; Publication No. US20050260205a1
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.

```

```

; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-273681
; CURRENT APPLICATION NUMBER: US/11/139,499
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: US/09/576,424
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-139-499-6

```

```

Query Match      83.5%; Score 1029; DB 7; Length 239;
Best Local Similarity 83.3%; Pred. No. 2,6e-62;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

```

```

QY 1 MCLPRL-VMFMIPASSDVLMTQTLPLVSLGDQASISCRSGQIVHNGNTYLEW 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MSLPQLGLLLCVPGSGEVMTQSPSLPTTPESPASISCRSGSLKHSNGDTFLSW 60
QY 60 YQKQSPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAP 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 YQKQSPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAP 120
QY 120 YTFGGGTLEIK-TAAPSVPFIPPSDQKSGTASVCLLNFPYPRKAVQKVDNALQ 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 PFGGQTKVEIKRTVAAPSVFIFPPSDQKSGTASVCLLNFPYPRKAVQKVDNALQ 180
QY 179 SGNQSVTEBQSKSTYSLSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 SGNQSVTEBQSKSTYSLSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 239

```

RESULT 3

```

US-11-080-587-8
; Sequence 8, Application US/11080587
; Publication No. US20060002942A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Calicheamicin Conjugates
; FILE REFERENCE: AM101462
; CURRENT APPLICATION NUMBER: US/11/080,587
; CURRENT FILING DATE: 2005-03-15
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Human/murine chimera
US-11-080-587-8

```

```

Query Match      79.6%; Score 980.5; DB 7; Length 219;
Best Local Similarity 84.5%; Pred. No. 4e-59;
Matches 185; Conservative 15; Mismatches 18; Indels 1; Gaps 1;

```

```

QY 20 DVLMTQTLPLVSLGDQASISCRSGQIVHNGNTYLEWYQKQSPKLLIYKVSNGF 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DQKQSPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAP 60
QY 80 SGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAPYTFGGGTLEIK-TAAPSVP 138

```

```

DB 61 SGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAPYTFGGGTLEIK-TAAPSVP 120
QY 139 FIFPSDQKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQSVTEBQSKSTYSL 198
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 FIFPSDQKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQSVTEBQSKSTYSL 180
QY 199 SSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 SSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 219

```

RESULT 4

```

US-11-158-505-1
; Sequence 1, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAMN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: T1N-031
; CURRENT APPLICATION NUMBER: US/11/158,505
; CURRENT FILING DATE: 2005-06-21
; PRIOR APPLICATION NUMBER: 60/582,181
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; REAGENT:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
; OTHER INFORMATION: antibody light chain construct
US-11-158-505-1

```

```

Query Match      77.2%; Score 951; DB 7; Length 238;
Best Local Similarity 76.2%; Pred. No. 3.9e-57;
Matches 183; Conservative 24; Mismatches 25; Indels 2; Gaps 2;

```

```

QY 5 VLLVLMFMIPASSDVLMTQTLPLVSLGDQASISCRSGQIVHNGNTYLEWYQK 64
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 6 ILVAVLLMVPGSTDIWVTQSPDLSLAVSLGRATINCKASQSVY-DGDSYNNYQGR 64
QY 65 QGSPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAPYTRG 124
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 65 GQPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAPYTRG 124
QY 125 GTKLEIK-TAAPSVPFIPPSDQKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQ 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 125 GTKVEIKRTVAAPSVFIFPPSDQKSGTASVCLLNFPYPRKAVQKVDNALQSGNSQ 184
QY 184 ESVTEBQSKSTYSLSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 237
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 185 ESVTEBQSKSTYSLSTLTSKADYERKHKYACEVTHQGLSSPYTKSFNRGEC 238

```

RESULT 5

```

US-11-158-505-3
; Sequence 3, Application US/11158505
; Publication No. US20060002921A1
; GENERAL INFORMATION:
; APPLICANT: WINSOR-HINES, DAMN
; APPLICANT: RAO, PATRICIA
; APPLICANT: RINGLER, DOUGLAS J
; APPLICANT: PONATH, PAUL
; TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
; TITLE OF INVENTION: INDUCTION IN PRIMATES
; FILE REFERENCE: T1N-031
; CURRENT APPLICATION NUMBER: US/11/158,505

```

```

QY 20 DVLMTQTLPLVSLGDQASISCRSGQIVHNGNTYLEWYQKQSPKLLIYKVSNGF 79
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 DQKQSPKLLIYKVSNGFSGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAP 60
QY 80 SGVDRFSGSGGTDFTLTKISRYEADLVGYCCFGTHAPYTFGGGTLEIK-TAAPSVP 138

```

[illegible]

RESULT 8
US-11-158-505-9
Sequence 9, Application US/11158505
Publication No. US20060002921A1
GENERAL INFORMATION:
APPLICANT: WINSOR-HINES, DAWN
APPLICANT: RAO, PATRICIA
APPLICANT: RINGLER, DOUGLAS J
APPLICANT: PONATH, PAUL
TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
FILE REFERENCE: TLN-031
CURRENT APPLICATION NUMBER: US/11/158, 505
CURRENT FILING DATE: 2005-06-21
PRIOR APPLICATION NUMBER: 60/582,181

```

? PRIOR FILING DATE: 2004-06-22
? NUMBER OF SEQ ID NOS: 76
? SOFTWARE: PatentIn Ver. 3.3
? SEQ ID NO 9
? LENGTH: 238
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
? OTHER INFORMATION: antibody light chain construct
? US-11-158-505-9

```

Query Match	76.4%;	Score 941;	DB 7;	Length 238;
Best Local Similarity	77.8%;	Pred. No. 1.8e-56;		
Matches 182;	Conservative 24;	Mismatches 26;	Indels 2;	Gaps 2;

[illegible]

RESULT 9

```

: Sequence 11, Application US/11158505
: Publication No. US20060002921A1
: GENERAL INFORMATION:
: APPLICANT: WINSOR-HINES, DAMN
: APPLICANT: RAO, PATRICIA
: APPLICANT: RINGLEY, DOUGLAS J
: APPLICANT: PONATH, PAUL
: TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
: TITLE OF INVENTION: INDUCTION IN PRIMATES
: FILE REFERENCE: TLN-031
: CURRENT APPLICATION NUMBER: US/11/158,505
: CURRENT FILING DATE: 2005-06-21
: PRIOR APPLICATION NUMBER: 60/582,181
: PRIOR FILING DATE: 2004-06-22
: NUMBER OF SEQ ID NOS: 76
: SOFTWARE: PatentIn Ver. 3.3
: SEQ ID NO 11
:
: LENGTH: 238
: TYPE: RPT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
: US-11-158-505-11

```

Query Match	76.4%	Score 941;	DB 7;	Length 238;
Best Local Similarity	77.8%;	Pred. NO. 1.8e-56;		
Matches 182;	Conservative 24;	Mismatches 26;	Indels 2;	Gaps 2

```
QY      5 VRLVLAMFMIASSSDVLTMTQPLSLPYSLSGDAQASICRSSQITVHSNNTYLEWYLQKP 64
      : | | : | : : | | : | | | | : : : | : : : | : : | | | |
Db      6 ILLWVLLWLVPGSTGDIWVTGSPDLSLWISGERATINCKASGSVDY-DGDSYNNWYQQKP 64
```

```

Qy      65 GQSPKLLIYKVISNRFSGVPPDRISGGSGSTDTIKISRLAEADGVVYFQGTAPPTFGG 12
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      65 GQPPKLLIYVANSLSGVPDRISGSGSTDTLTISLQAEADVAVVYQQSLQDPPTFGG 12

```

QY 125 GTKLEIK-TAAAPSVFI FPPSDEQLKSGTASVCLNNFY PREAKVQWKVDNALQSGNSQ 183

Db 125 GTVKEIKRTVALSVATPPPSDQKSGSTASVCLNNFFPRKAKVQMKVDNALQSGNSQ 18

Qy 184 ESVTEDSKDSSTYSLSSTLTLLSKADYERKRYACEVTHQGLSSPYTSSFNNGEC 237

Db 185 ESVTEDSKDSSTYSLSSTLTLLSKADYERKRYACEVTHQGLSSPYTSSFNNGEC 238

RESULT 10
US-11-158

; Sequence 17, Application US/11158505
; Publication No. US20060002921A1
; Publication No. US20060002921A1

```

1  APPLICANT:  WINSOR-HINES, DAWN
2  APPLICANT:  RAO, PATRICIA
3  APPLICANT:  RINGLER, DOUGLAS J
4  APPLICANT:  POMATH, PAUL
5  TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
6  TITLE OF INVENTION: INDUCTION IN PRIMATES
7  FILE REFERENCE: TLN-031
8  CURRENT APPLICATION NUMBER: US/11/158,505
9  CURRENT FILING DATE: 2005-06-21
10 PRIOR APPLICATION NUMBER: 60/582,181
11 PRIOR FILING DATE: 2004-06-22
12 NUMBER OF SEQ ID NOS: 76
13 SOFTWARE: PatentIn Ver. 3.3
14 SEQ ID NO 17
15 LENGTH: 238
16 TYPE: PRT
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: Description of Artificial Sequence: Synthetic TRX1
20 OTHER INFORMATION: antibody light chain sequence
21 US-11-158-505-17

```

Query

	Query Match	76.4%	Score 941	DB 7	Length 238
	Best Local Similarity	77.8%	Pred. No. 1,8e-56		
	Matches 182	Conservative 24	Mismatches 26	Indels 2	Gaps 2
QY	5	VRLLVLMFMWIPASSSDVIMTQTPFLSPVSLGDQASISCRSGGTIYHSKNTYLTMYLQRP	64		
DB	6	ILVLLVLLMFMWIPASSSDVIMTQTPFLSPVSLGDQASISCRSGGTIYHSKNTYLTMYLQRP	64		
QY	65	QOSPFLILYKYSNRSRGVDPDRFSGSGSGDFFLKTSRVABDLGVYVCFQGTAPYTFQ	124		
DB	65	QQPFLLIYVANSNLSGVPPDRFSGSGSGDFTLTLSLQAEVAVYYCCQSLQDPPTFQ	124		
QY	125	GTKLEIK-TAAAPSVYIFPPSDDEQLKSGTASVCLINFPYPREATQVMKDALOSGNSQ	183		
DB	125	GTKVEIKRTVVALSVYIFPPSDDEQLKSGTASVCLINFPYPREAQVMKDALOSGNSQ	184		
QY	184	ESVYRQDSKDSYSLSTLLSKADYKHKYKVAACEVTHQGLSPPTKSNRQRC	237		
DB	185	ESVYRQDSKDSYSLSTLLSKADYKHKYKVAACEVTHQGLSPPTKSNRQRC	238		

RESULT 11

US-11-158-200-15
; Sequence 19, Application US/11158505
; Publication No. US20060002921A1

/ GENERAL INFORMATION:
 / APPLICANT: MINSOR-HINES, DAWN
 / APPLICANT: RAO, PATRICIA
 / APPLICANT: RINGLER, DOUGLAS J
 / APPLICANT: PONATH, PAUL
 / TITLE OF INVENTION: OPTIMIZED DOSING OF ANTI-CD4 ANTIBODIES FOR TOLERANCE
 / TITLE OF INVENTION: INDUCTION IN PRIMATES
 / FILE REFERENCE: TLM-031

;; CURRENT APPLICATION NUMBER: US/11/15
;; CURRENT FILING DATE: 2005-06-21
;; PRIOR APPLICATION NUMBER: 60/582,181

; NUMBER OF SEQ ID NOS: 76

Publication No. US20050287136A1
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MEILLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
TITLE OF INVENTION: CORVALLAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3

```

; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 67
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-67
```

```

Query Match 74.6%; Score 919; DB 7; Length 233;
Best Local Similarity 74.1%; Pred. No. 5.1e-55;
Matches 177; Conservative 31; Mismatches 23; Indels 8; Gaps 3;
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```

QY 1 MCLPYRLI-VLMFWIPASSSDVLMQTPLSLPVSLGDOASISCRSSQTIHNSNGNTYLEW 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 METPAQLFLFLMLPDTTGRIVLQSPGTLSLSPGERATLSCRSQI-----SSYLAW 54

QY 60 YLQKPGQSPKLLIYKVSNRFGVPPRFGSGSGSDTFTLKISRVEAEDLGVYYCFQGTAP 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 55 YQKPGQAPRLIYQASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYCQYGISP 114

QY 120 YTFGGGTLEIK-TAAPSVFIIPPSDQOLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 115 YQKPGQAPRLIYQASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYCQYGISP 174

QY 179 SGNQSESVTEBDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 237
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 SGNQSESVTEBDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 233
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RESULT 15

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US-11-128-900-14
; Sequence 14, Application US/11/128,900
; Publication No. US20050287136A1
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI DIV3
; CURRENT APPLICATION NUMBER: US/11/128,900
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: US 10/776649
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: US 10/612497
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: 2003-07-01
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: US 60/113647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-900-14
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Query Match 74.4%; Score 916; DB 7; Length 235;
Best Local Similarity 73.6%; Pred. No. 8.1e-55;
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Matches 176; Conservative 33; Mismatches 24; Indels 6; Gaps 3;

QY 1 MCLPYRLI-VLMFWIPASSSDVLMQTPLSLPVSLGDOASISCRSSQTIHNSNGNTYLEW 59
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 METPAQLFLFLMLPDTTGRIVLQSPGTLSLSPGERATLSCRSQI-----SSYLAW 56

QY 60 YLQKPGQSPKLLIYKVSNRFGVPPRFGSGSGSDTFTLKISRVEAEDLGVYYCFQGTAP 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 57 YQKPGQAPRLIYQASSRATGIPDRFSGSGSGTDFTLISRLEPEDFAVYYCQYGISP 116

QY 120 YTFGGGTLEIK-TAAPSVFIIPPSDQOLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 117 YTFGGGTLEIK-TAAPSVFIIPPSDQOLKSGTASVCLNNFYPREAKVQMKVDNALQ 176

QY 179 SGNQSESVTEBDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 237
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 177 SGNQSESVTEBDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSPVTKSFNRGEC 235
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Search completed: January 24, 2006, 19:13:53
Job time : 12.5279 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:56:50 ; Search time 57.9785 seconds
(without alignments)
1707.969 Million cell updates/sec

Title: US-10-828-782A-16
Perfect score: 1232
Sequence: 1 MKLPVRLIVLFWIPASSSD.....EVTGGLSSPYTKSFNRGEC 237

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1232	100.0	237	5	US-10-828-782A-16
2	1164.5	94.5	238	5	US-10-497-475-19
3	1089.5	88.4	219	5	US-10-880-028-45
4	1089.5	88.4	219	5	US-10-880-320-45
5	1069.5	86.8	219	5	US-10-497-475-11
6	1049	85.1	239	6	US-11-031-485-36
7	1046	84.9	239	6	US-11-031-485-44
8	1043	84.7	239	6	US-11-031-485-44
9	1043	84.7	242	3	US-09-726-258-42
10	1039	84.3	239	4	US-10-292-088-32
11	1032	83.8	239	4	US-10-292-088-40
12	1030	83.6	220	4	US-10-737-208A-5
13	1030	83.6	220	6	US-11-040-071-2
14	1030	83.6	239	4	US-10-292-088-56
15	1029	83.5	239	3	US-09-758-173-6
16	1029	83.5	239	3	US-09-948-429B-6
17	1029	83.5	239	4	US-10-124-905-6
18	1029	83.5	239	4	US-10-124-807-6
19	1029	83.5	239	4	US-10-291-532-6
20	1029	83.5	239	4	US-10-428-408A-28
21	1029	83.5	239	4	US-10-428-894-28
22	1029	83.5	239	4	US-10-699-874-28
23	1029	83.5	239	5	US-10-986-780-6
24	1028.5	83.5	219	4	US-10-226-435A-11
25	1028.5	83.5	219	4	US-10-487-322-11
26	1028.5	83.5	219	5	US-10-487-326-11
27	1028.5	83.5	219	5	US-10-486-908-11

28	1028.5	83.5	219	5	US-10-512-527-11	Sequence 11, Appl
29	1028	83.4	239	4	US-10-292-088-16	Sequence 16, Appl
30	1025.5	83.2	238	6	US-11-031-485-40	Sequence 40, Appl
31	1025	83.2	247	4	US-10-466-164-69	Sequence 69, Appl
32	1024	83.1	239	6	US-11-131-648-21	Sequence 21, Appl
33	1024	83.1	239	6	US-11-131-648-51	Sequence 51, Appl
34	1023	83.0	239	4	US-10-292-088-102	Sequence 102, App
35	1022	83.0	239	4	US-10-292-088-8	Sequence 8, Appl
36	1021	82.9	239	6	US-11-031-485-66	Sequence 66, Appl
37	1020	82.8	239	4	US-10-404-724-39	Sequence 39, Appl
38	1020	82.8	239	4	US-10-292-088-64	Sequence 64, Appl
39	1020	82.8	239	4	US-10-292-088-80	Sequence 80, Appl
40	1020	82.8	239	5	US-10-816-276-35	Sequence 35, Appl
41	1019	82.7	239	4	US-10-404-724-12	Sequence 12, Appl
42	1019	82.7	239	4	US-10-404-724-47	Sequence 47, Appl
43	1019	82.7	239	5	US-10-816-276-8	Sequence 8, Appl
44	1019	82.7	239	5	US-10-816-276-43	Sequence 43, Appl
45	1019	82.7	239	6	US-11-031-485-32	Sequence 32, Appl

ALIGNMENTS

```

RESULT 1
US-10-828-782A-16
; Sequence 16, Application US/10828782A
; Publication No. US20040242848A1
; GENERAL INFORMATION:
; APPLICANT: Owens, S. Michael.
; TITLE OF INVENTION: Mouse/Human Chimeric Anti-Phencyclidine
; TITLE OF INVENTION: Antibody And Uses Thereof
; FILE REFERENCE: D6508
; CURRENT FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US/10/828,782A
; PRIOR FILING DATE: 2003-04-21
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 16
; LENGTH: 237
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of anti-PCP
; OTHER INFORMATION: ch-mab6B5 light chain.
US-10-828-782A-16

Query Match          100.0%; Score 1232; DB 5; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e-58;
Matches 237; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MKLPVRLIVLFWIPASSSDVLTMTQPLSPVSLDQASISCRSSQTVHSNGNTLYEWY 60
DB      1 MKLPVRLIVLFWIPASSSDVLTMTQPLSPVSLDQASISCRSSQTVHSNGNTLYEWY 60

QY      1 LKPKQSSKLLIYKSNPFGVDFRSGSGSTDTLKIISREADLGYVYFOGHAPY 120
DB      1 LKPKQSSKLLIYKSNPFGVDFRSGSGSTDTLKIISREADLGYVYFOGHAPY 120

QY      121 TFGGSKTKEIKTAAAPVFIFPPSDEQKSGTASVYCLNNFYPREAKQWVDNALOSG 180
DB      121 TFGGSKTKEIKTAAAPVFIFPPSDEQKSGTASVYCLNNFYPREAKQWVDNALOSG 180

QY      121 TFGGSKTKEIKTAAAPVFIFPPSDEQKSGTASVYCLNNFYPREAKQWVDNALOSG 180
DB      121 TFGGSKTKEIKTAAAPVFIFPPSDEQKSGTASVYCLNNFYPREAKQWVDNALOSG 180

QY      181 NSQESVTEQDSKDSSTYSLSSTLTLSKADYERKRVYACEVTHQGLSSPYTKSFNRGEC 237
DB      181 NSQESVTEQDSKDSSTYSLSSTLTLSKADYERKRVYACEVTHQGLSSPYTKSFNRGEC 237

RESULT 2
US-10-497-475-19
; Sequence 19, Application US/10497475
; Publication No. US20050142131A1
; GENERAL INFORMATION:

```

```
/ APPLICANT: Paul Robert Hinton
/ APPLICANT: Maximiliano J. Vaequez
/ TITLE OF INVENTION: Humanized Antibodies
/ FILE REFERENCE: X-14819
/ CURRENT APPLICATION NUMBER: US/10/497,475
/ CURRENT FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US 60/287,653
/ PRIOR FILING DATE: 2001-04-30
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 19
/ LENGTH: 238
/ TYPE: PRT
/ ORGANISM: humanized antibody
US-10-497-475-19

Query Match          94.5%; Score 1164.5; DB 5; Length 238;
Best Local Similarity 93.7%; Pred. No. 5.7e-55;
Matches 223; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 1 MKLPVRLVLMFWIPASSSDVMTQTPLSPVSLGDAISCRSSQTIIVHNGNTYLEWY 60
DB 1 MKLPVRLVLMFWIPASSSDVMTQSPVSLGDAISCRSSQTIIVHNGNTYLEWY 60
QY 61 LQKPGQSPKLLIYKVSNNRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGTHAPY 120
DB 61 LQKPGQSPKLLIYKVSNNRSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGTHAPY 120
QY 121 TFGGGTKLEIK-TAAAPSVFIPEPPSDGDKSGTASVCLNNFYPREAKVQMKVDNALQS 179
DB 121 TFGGGTKLEIK-TAAAPSVFIPEPPSDGDKSGTASVCLNNFYPREAKVQMKVDNALQS 180
QY 180 GNSQSVTEQDSKDSITSLSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 237
DB 181 GNSQSVTEQDSKDSITSLSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 238

RESULT 3
US-10-880-028-45
/ Sequence 45, Application US/10880028
/ Publication No. US20050163782A1
/ GENERAL INFORMATION:
/ APPLICANT: BRASLAWSKY, Gary R.
/ APPLICANT: GLASER, Scott
/ APPLICANT: YANG, Tzung-Hong
/ APPLICANT: HOPF, Jennifer
/ APPLICANT: CHINN, Paul
/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES
/ FILE REFERENCE: IDV-001
/ CURRENT APPLICATION NUMBER: US/10/880,028
/ CURRENT FILING DATE: 2004-06-28
/ PRIOR APPLICATION NUMBER: 60/483877
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/508810
/ PRIOR FILING DATE: 2003-10-03
/ PRIOR APPLICATION NUMBER: 60/515351
/ PRIOR FILING DATE: 2003-10-28
/ PRIOR APPLICATION NUMBER: 60/516030
/ PRIOR FILING DATE: 2003-10-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 219
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-880-028-45

Query Match          88.4%; Score 1089.5; DB 5; Length 219;
Best Local Similarity 95.9%; Pred. No. 5.3e-51;
Matches 210; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
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```
QY 20 DVLMTQTPLSLPVSLGDAISCRSSQTIIVHNGNTYLEWYLOKPGQSPKLLIYVSNRF 79
DB 1 DFLMTQTPLSLPVSIGDQASISCRSSQSIIVHNGNTYLEWYLOKPGQSPKLLIYVSNRF 60
QY 80 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGTHAPYTFGGGTLEIK-TAAAPSV 138
DB 61 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGSHVPLTFGAGTKLEIKRTVTAAPSV 120
QY 139 FIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITSL 198
DB 121 FIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITSL 180
QY 199 SSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 219

RESULT 4
US-10-880-320-45
/ Sequence 45, Application US/10880320
/ Publication No. US20050163783A1
/ GENERAL INFORMATION:
/ APPLICANT: BRASLAWSKY, Gary R.
/ APPLICANT: GLASER, Scott
/ APPLICANT: YANG, Tzung-Hong
/ APPLICANT: HOPF, Jennifer
/ APPLICANT: CHINN, Paul
/ TITLE OF INVENTION: PURIFICATION AND PREFERENTIAL SYNTHESIS
/ TITLE OF INVENTION: OF BINDING POLYPEPTIDES
/ FILE REFERENCE: IDV-001
/ CURRENT APPLICATION NUMBER: US/10/880,320
/ CURRENT FILING DATE: 2004-06-28
/ PRIOR APPLICATION NUMBER: 60/483877
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/508810
/ PRIOR FILING DATE: 2003-10-03
/ PRIOR APPLICATION NUMBER: 60/515351
/ PRIOR FILING DATE: 2003-10-28
/ PRIOR APPLICATION NUMBER: 60/516030
/ PRIOR FILING DATE: 2003-10-30
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 219
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-880-320-45

Query Match          88.4%; Score 1089.5; DB 5; Length 219;
Best Local Similarity 95.9%; Pred. No. 5.3e-51;
Matches 210; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 20 DVLMTQTPLSLPVSLGDAISCRSSQTIIVHNGNTYLEWYLOKPGQSPKLLIYVSNRF 79
DB 1 DFLMTQTPLSLPVSIGDQASISCRSSQSIIVHNGNTYLEWYLOKPGQSPKLLIYVSNRF 60
QY 80 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGTHAPYTFGGGTLEIK-TAAAPSV 138
DB 61 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYYCFOGSHVPLTFGAGTKLEIKRTVTAAPSV 120
QY 139 FIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITSL 198
DB 121 FIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITSL 180
QY 199 SSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SSTLTLSKADYEKKHVVACEVTHQGLSSPVTKSFNRGEC 219

RESULT 5
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US-10-497-475-11
; Sequence 11, Application US/10497475
; Publication No. US20050142131A1
; GENERAL INFORMATION:
; APPLICANT: Paul Robert Hinton
; APPLICANT: Maximiliano J. Vasquez
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: US/10/497,475
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/287,653
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: humanized antibody
US-10-497-475-11

Query Match 86.8%; Score 1069.5; DB 5; Length 219;
Best Local Similarity 93.2%; Pred. No. 6.2e-50;
Matches 204; Conservative 8; Mismatches 6; Indels 1; Gaps 1;

QY 20 DVLMTQPLSLPVSIGDQASISCRSSQTIHNSNGTYLEWYLQKPGSPKLLIYKVSNR 79
DB 1 DVMWQSPSLSPVTLGQPASISCRSSQNIHNSNGTYLEWYLQKPGSPKLLIYKVSNR 60
QY 80 SGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAPYFGGCTLEIK-TAAAPSV 138
DB 61 SGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGHVPLFGGCTYVEIKRTVAAPSV 120
QY 139 FIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQSGNSQESTYEDDSKSTYS 198
DB 121 FIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQSGNSQESTYEDDSKSTYS 180
QY 199 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 6
US-11-031-485-36
; Sequence 36, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCH, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PP6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 36
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-36

Query Match 85.1%; Score 1049; DB 6; Length 239;
Best Local Similarity 84.1%; Pred. No. 8.3e-49;
Matches 201; Conservative 19; Mismatches 17; Indels 2; Gaps 2;

QY 1 MRLPVRLI-VLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 59
DB 1 MRLPVRLI-VLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 60

QY 60 YLQKPGSPKLLIYKVSNRFGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 119
DB 61 YLQKPGSPKLLIYKVSNRFGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 120
QY 120 YTPGGTLEIK-TAAAPSVFIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQ 178
DB 121 WTPGGTVEIKRTVAAPSVFIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQ 180
QY 179 SGNQSEYSTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SGNQSEYSTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7
US-11-031-485-68
; Sequence 68, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCH, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PP6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 68
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-68

Query Match 84.9%; Score 1046; DB 6; Length 239;
Best Local Similarity 84.5%; Pred. No. 1.2e-48;
Matches 202; Conservative 18; Mismatches 17; Indels 2; Gaps 2;

QY 1 MRLPVRLI-VLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 59
DB 1 MRLPVRLI-VLMFWIPASSSDVLMQTPLSLPVSIGDQASISCRSSQTIHNSNGTYLEW 60
QY 60 YLQKPGSPKLLIYKVSNRFGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 119
DB 61 YLQKPGSPKLLIYKVSNRFGVDRFSGSGSGTDFTLKISRVEAEDGAVYYCFQGTAP 120
QY 120 YTPGGTLEIK-TAAAPSVFIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQ 178
DB 121 WTPGGTVEIKRTVAAPSVFIFPPSDQOLSKSTAVVCLINNFYPRKAVQWKVDNALQ 180
QY 179 SGNQSEYSTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 181 SGNQSEYSTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8
US-11-031-485-44
; Sequence 44, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMANN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCH, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCAM
; FILE REFERENCE: ABX-PP6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490

/ PRIOR FILING DATE: 2004-01-09
 / NUMBER OF SEQ ID NOS: 147
 / SOFTWARE: Patent In Ver. 3.3
 / SEQ ID NO 44
 / LENGTH: 239
 / TYPE: prt
 / ORGANISM: Homo sapiens
 US-11-031-485-44

Query Match 84.7%; Score 1043; DB 6; Length 239;
 Best Local Similarity 84.1%; Pred. No. 1.7e-48;
 Matches 201; Conservative 19; Mismatches 17; Indels 2; Gaps 2;

QY 1 MCLPVRLL-VLMFWIPASSSDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPVRLL-VLMFWIPASSSDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 60
 QY 60 YLQKPGQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 119
 DB 61 YLQKPGQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 120
 QY 120 YTFGGGTLEIK-TAAPSVEFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 178
 DB 121 YTFGGGTLEIK-TAAPSVEFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 180
 QY 179 SGNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 237
 DB 181 SGNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 239

RESULT 9
 US-09-726-258-42
 / Sequence 42, Application US/09726258
 / Publication No. US20030021790A1

GENERAL INFORMATION:

/ APPLICANT: Genentech, Inc., Heei, Vanessa
 / APPLICANT: Koumenis, Iphigenia
 / APPLICANT: Leong, Steven R.
 / APPLICANT: Presta, Leonard G.
 / APPLICANT: Shatrokh, Zahra
 / APPLICANT: Zapata, Gerardo A.
 / TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
 / TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
 / NUMBER OF SEQUENCES: 72
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 1 DNA Way
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080

/ COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPatIn (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/09/726,258
 / FILING DATE:

/ CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 09/234,182
 / FILING DATE:

/ PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 60/094003
 / FILING DATE: 24-JUL-1998
 / ATTORNEY/AGENT INFORMATION:

/ NAME: Love, Richard B.
 / REGISTRATION NUMBER: 34,659
 / REFERENCE/DOCKET NUMBER: P1085R4-1A
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650/225-5530
 / TELEFAX: 650/952-9881

/ INFORMATION FOR SEQ ID NO: 42:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 242 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 US-09-726-258-42

Query Match 84.7%; Score 1043; DB 3; Length 242;
 Best Local Similarity 86.4%; Pred. No. 1.7e-48;
 Matches 203; Conservative 12; Mismatches 16; Indels 4; Gaps 2;

QY 7 LILVFWIPASS---SDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 63
 DB 8 LILVFWIPASS---SDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 67
 QY 64 PQQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 123
 DB 68 PQQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 127
 QY 124 GGTLEIK-TAAPSVEFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 182
 DB 128 AGTKLEIKRAVAAPVFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 187
 QY 183 QSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 237
 DB 188 QSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 242

RESULT 10
 US-10-292-088-32
 / Sequence 32, Application US/10292088
 / Publication No. US20030211100A1

GENERAL INFORMATION:

/ APPLICANT: BEDIAN, VAHE
 / APPLICANT: GLADUE, RONALD P.
 / APPLICANT: CORVALAN, JOSE
 / APPLICANT: JIA, XIAO-CHI
 / APPLICANT: FENG, XIAO
 / TITLE OF INVENTION: ANTIBODIES TO CD40
 / FILE REFERENCE: ABX-PF/3 US
 / CURRENT APPLICATION NUMBER: US/10/292,088
 / PRIOR FILING DATE: 2003-03-14
 / PRIOR APPLICATION NUMBER: 60/348,980
 / PRIOR FILING DATE: 2001-11-09
 / NUMBER OF SEQ ID NOS: 147
 / SOFTWARE: Patent In Ver. 2.1
 / SEQ ID NO 32
 / LENGTH: 239
 / TYPE: prt
 / ORGANISM: Homo sapiens
 US-10-292-088-32

Query Match 84.3%; Score 1039; DB 4; Length 239;
 Best Local Similarity 83.7%; Pred. No. 2.8e-48;
 Matches 200; Conservative 17; Mismatches 20; Indels 2; Gaps 2;

QY 1 MCLPVRLL-VLMFWIPASSSDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPVRLL-VLMFWIPASSSDVLMOTPLSLPVSLGDQASISCRSSQTIHNSGNTYLEM 60
 QY 60 YLQKPGQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 119
 DB 61 YLQKPGQSPKLLIYKSNRFGSVPRFSGSGGTDTLTLSRVEADLVVYCFQGTNAP 120
 QY 120 YTFGGGTLEIK-TAAPSVEFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 178
 DB 121 YTFGGGTLEIK-TAAPSVEFIFFPSDEQLKSGTASVCLNNFYPRKAVQMKVDNALQ 180
 QY 179 SGNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 237
 DB 181 SGNSQSVTEQDSKSTYSLSSTLTLSKADYKHKYACEVTHQGLSPVTSFNRGEC 239

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RESULT 11
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match
Best Local Similarity 83.8%; Score 1032; DB 4; Length 239;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MCLPRL-VIMFWIPASSDVLMTQTPISLPSVLSGDQASISCRSSQTIHNSNGTYLHW
DB 1 MCLPRL-VIMFWIPASSDVLMTQTPISLPSVLSGDQASISCRSSQTIHNSNGTYLHW 59
60 YLQKQSPKLLIYKVSNGVPPRFGSGSGCTPFTLKISVREABDLGVYTCFPGCTA 119
61 YLQKQSPKLLIYKVSNGVPPRFGSGSGCTPFTLKISVREABDLGVYTCFPGCTA 120
120 YFGGCTKLEIK-TAAPSVPFIFPPSDDEQLKSGTASVCLNNFYPREAKVQMDNALQ 178
121 FTFGCTKADIKRTVAAPSVPFIFPPSDDEQLKSGTASVCLNNFYPREAKVQMDNALQ 180
QY 179 SGNQSESVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 237
DB 181 SGNQSESVTEODSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 239

RESULT 12
US-10-737-208A-5
; Sequence 5, Application US/10737208A
; Publication No. US20040203100A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Lo, Kin-Ming
; TITLE OF INVENTION: IMMUNOCYTOKINE SEQUENCES AND USES THEREOF
; FILE REFERENCE: LEX-023
; CURRENT APPLICATION NUMBER: US/10/737,208A
; CURRENT FILING DATE: 2003-12-16
; PRIOR APPLICATION NUMBER: US 60/433,945
; PRIOR FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 5
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Immunoglobulin light chain
US-10-737-208A-5

Query Match
Best Local Similarity 90.9%; Score 1030; DB 4; Length 220;
Matches 200; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 20 DVLMTQTPISLPSVLSGDQASISCRSSQTIHNSNGTYLHWYQLKQSPKLLIYKVSNGF 79
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DB 1 DVLMTQTPISLPSVTEGEBASISCRSSQSLVHNSNGTYLHWYQLKQSPKLLIHKVSNGF 60
QY 80 SGVPRFSGSGGTDFTLKISRVEAEDLGVYTCFPGCTA-PYFGGCTKLEIK-TAAPS 137
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYTCFPGCTA-PYFGGCTKLEIK-TAAPS 120
QY 138 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMDNALQSGNSQESVTEODSKDSTYS 197
DB 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMDNALQSGNSQESVTEODSKDSTYS 180
QY 198 LSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 237
DB 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 220

RESULT 13
US-11-040-071-2
; Sequence 2, Application US/11040071
; Publication No. US20050202021A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen D.
; APPLICANT: Anti-Cancer Antibodies with Reduced Complement Fixation
; FILE REFERENCE: LEX-031
; CURRENT APPLICATION NUMBER: US/11/040,071
; CURRENT FILING DATE: 2005-01-21
; PRIOR APPLICATION NUMBER: US 60/538,348
; PRIOR FILING DATE: 2004-01-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 2
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-040-071-2

Query Match
Best Local Similarity 90.9%; Score 1030; DB 6; Length 220;
Matches 200; Conservative 8; Mismatches 10; Indels 2; Gaps 2;

QY 20 DVLMTQTPISLPSVLSGDQASISCRSSQTIHNSNGTYLHWYQLKQSPKLLIYKVSNGF 79
DB 1 DVLMTQTPISLPSVTEGEBASISCRSSQSLVHNSNGTYLHWYQLKQSPKLLIHKVSNGF 60
QY 80 SGVPRFSGSGGTDFTLKISRVEAEDLGVYTCFPGCTA-PYFGGCTKLEIK-TAAPS 137
DB 61 SGVPRFSGSGGTDFTLKISRVEAEDLGVYTCFPGCTA-PYFGGCTKLEIK-TAAPS 120
QY 138 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMDNALQSGNSQESVTEODSKDSTYS 197
DB 121 VFIPPSDEQLKSGTASVCLNNFYPREAKVQMDNALQSGNSQESVTEODSKDSTYS 180
QY 198 LSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 237
DB 181 LSTLTLSKADYKHKVYACEVTHQGLSSPVTGSFNRGEC 220

RESULT 14
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: PENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
```

NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 56
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-088-56

Query Match 83.6%; Score 1030; DB 4; Length 239;
Best Local Similarity 83.7%; Pred. No. 8.5e-48;
Matches 200; Conservative 16; Mismatches 21; Indels 2; Gaps 2;

QY 1 MSLPRL-L-VLMFWIPASSDVLMTQPLSLPVSIGDQASISCRSSQTIHNSNGNTYLEW 59
DB 1 MSLPRLGLLILCVPGSSGEVMTQSPLSLPTITGEPASISCRSSQSIKHSNGDTFLSM 60
QY 60 YIQKQSPKLLIYVSNRFGVPPRFGSGSGGTPTLKSIVAEADLVGYVCFQGTAP 119
DB 61 YIQKQSPKLLIYVSNRFGVPPRFGSGSGGTPTLKSIVAEADLVGYVCFQGTAP 120
QY 120 YTFGGGTLEIK-TAAPSVEIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
DB 121 PTFGGGTVEIKRTVTAAPSVEIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 180
QY 179 SGNQSESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTSFNRGEC 237
DB 181 SGNQSESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTSFNRGEC 239

RESULT 15

US-09-758-173-6
Sequence 6, Application US/09758173
Publication No. US20010024648A1
GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,173
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: Protein
US-09-758-173-6

Query Match 83.5%; Score 1029; DB 3; Length 239;
Best Local Similarity 83.3%; Pred. No. 9.6e-48;
Matches 199; Conservative 19; Mismatches 19; Indels 2; Gaps 2;

QY 1 MSLPRL-L-VLMFWIPASSDVLMTQPLSLPVSIGDQASISCRSSQTIHNSNGNTYLEW 59
DB 1 MSLPRLGLLILCVPGSSGEVMTQSPLSLPTITGEPASISCRSSQSIKHSNGDTFLSM 60
QY 60 YIQKQSPKLLIYVSNRFGVPPRFGSGSGGTPTLKSIVAEADLVGYVCFQGTAP 119
DB 61 YIQKQSPKLLIYVSNRFGVPPRFGSGSGGTPTLKSIVAEADLVGYVCFQGTAP 120
QY 120 YTFGGGTLEIK-TAAPSVEIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 178
DB 121 PTFGGGTVEIKRTVTAAPSVEIFPPSDQLKSGTASVCLNNFYPREAKVQMKVDNALQ 180
QY 179 SGNQSESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTSFNRGEC 237
DB 181 SGNQSESVTEQDSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSPVTSFNRGEC 239

Search completed: January 24, 2006, 19:13:07
Job time : 58.9785 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 24, 2006, 18:44:45 ; Search time 77.3047 Seconds
(without alignments)

2163.001 Million cell updates/sec

Title: US-10-828-782A-16

Perfect score: 1232

Sequence: 1 MKLTVRLVLMFWIPASSSD.....EVTHQGLSSPYTKSPNRGEC 237

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	86.0	239	08TCD0_HUMAN	08TCD0 homo sapien
2	1045	84.8	239	06P491_HUMAN	06P491 homo sapien
3	1032	83.8	239	08NEKO_HUMAN	08NEKO homo sapien
4	1021.5	82.9	240	06PIH6_HUMAN	06PIH6 homo sapien
5	920.5	74.7	236	06PIH8_HUMAN	06PIH8 homo sapien
6	911	73.9	235	06GMV9_HUMAN	06GMV9 homo sapien
7	907.5	73.7	236	06PS88_HUMAN	06PS88 homo sapien
8	901.5	73.2	236	06GMX8_HUMAN	06GMX8 homo sapien
9	900	73.1	235	06P492_HUMAN	06P492 homo sapien
10	896.5	72.8	236	06GMW1_HUMAN	06GMW1 homo sapien
11	894.5	72.6	236	06GMX0_HUMAN	06GMX0 homo sapien
12	893.5	72.5	236	06PIH7_HUMAN	06PIH7 homo sapien
13	892	72.4	235	06GMW0_HUMAN	06GMW0 homo sapien
14	884.5	71.8	234	072473_HUMAN	072473 homo sapien
15	875.5	71.1	236	0502W4_HUMAN	0502W4 homo sapien
16	865.5	70.6	234	05EFB6_HUMAN	05EFB6 homo sapien
17	865.5	70.3	236	06PIH4_HUMAN	06PIH4 homo sapien
18	864.5	70.2	236	06PIH5_HUMAN	06PIH5 homo sapien
19	860.5	69.8	236	06GMX9_HUMAN	06GMX9 homo sapien
20	859.5	69.8	236	0723Y4_HUMAN	0723Y4 homo sapien
21	854.5	69.4	219	0652C0_MOUSE	0652C0 mus musculu
22	853.5	69.3	234	056919_HUMAN	056919 homo sapien
23	821.5	66.7	239	0588U8_MOUSE	0588U8 mus musculu
24	798.5	64.8	234	05XK44_MOUSE	05XK44 mus musculu
25	734	59.6	240	052164_MOUSE	052164 mus musculu
26	725	58.8	238	06C1S7_MOUSE	06C1S7 mus musculu
27	711.5	57.8	236	07M998_MOUSE	07M998 mus musculu
28	692.5	56.2	234	04K666_RAT	04K666 rattus norv
29	685.5	55.6	236	052195_MOUSE	052195 mus musculu
30	682	55.4	238	0588U4_MOUSE	0588U4 mus musculu
31	677.5	55.0	234	05M838_RAT	05M838 rattus norv

32	668	54.2	241	0632X4_MOUSE	0632X4 mus musculu
33	640.5	52.0	237	0569Y8_MOUSE	0569Y8 mus musculu
34	629.5	51.1	235	05XFX8_MOUSE	05XFX8 mus musculu
35	623.5	50.5	235	0588V6_MOUSE	0588V6 mus musculu
36	619.5	50.3	189	056917_HUMAN	056917 homo sapien
37	576.5	46.8	120	06P5R3_HUMAN	06P5R3 homo sapien
38	565	45.9	248	065207_MOUSE	065207 mus sp. b3
39	551.5	44.8	243	06NTU5_XENLA	06NTU5 xenopus lae
40	545	44.2	237	07S236_XENLA	07S236 xenopus lae
41	544	44.2	106	KAC_HUMAN	P01834 homo sapien
42	541.5	44.0	239	05HZC6_XENTR	05HZC6 xenopus tro
43	540.5	43.9	115	05F210_MOUSE	05F210 mus musculu
44	532	43.2	113	KV2G_MOUSE	P01631 mus musculu
45	529.5	43.0	133	KV2F_HUMAN	P06310 homo sapien

ALIGNMENTS

RESULT 1
ID 08TCD0_HUMAN PRELIMINARY; PRT; 239 AA.
AC 08TCD0;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltan E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lung;
RX Strausberg R.;
DT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1598223;
RA Hirabayashi Y., Munakata Y., Sasaki T., Sano H.;
RT "Variable regions of a human anti-DNA antibody O-81 possessing lupus
RT nephritis-associated idiotype";
RT Nucleic Acids Res. 20:2601-0(1992).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1551402;
RA Lauener-Rieske A., Huber C., Meindl A., Pargent W., Schable K.F.,
RA Thiede R., Zocher I., Zachau H.G.;

RT "The human immunoglobulin kappa locus. Characterization of the
 RT duplicated A regions.";
 RL Eur. J. Immunol. 22:1023-1029 (1992).
 RN (5)
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8256341;
 RT Klein R., Jaenichen R., Zachau H.G.;
 RL "Expressed human immunoglobulin kappa genes and their hypermutation.";
 RL Eur. J. Immunol. 23:3248-3262 (1993).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;
 RT Wagner S.D., Luzzatto L.;
 RL "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 RT distributed over a large portion of the V kappa locus and do not show
 RT somatic mutation.";
 RL Eur. J. Immunol. 23:391-397 (1993).
 DR EMBL, BC023362; AAH23362.1; -, mRNA.
 DR PIR, S32658; S22658.
 DR PIR, S34095; S34095.
 DR PIR, S40324; S40324.
 DR PIR, S40374; S40374.
 DR PIR, S42267; S42267.
 DR PIR, S42268; S42268.
 DR HSSP, P01834; 117Z.
 DR SMR, Q8TCD0; 21-237.
 DR InterPro, IPR007110; IG-like.
 DR InterPro, IPR003597; IG-cl.
 DR InterPro, IPR003006; IG_MHC.
 DR InterPro, IPR003596; IG_v.
 DR Pfam, PF07654; Cl-set; 1.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG_LIKE; 2.
 DR PROSITE, PS50290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein; Immunoglobulin domain.
 SQ SEQUENCE 239 AA; 26235 MW; FACDCA3803871D CRC64;

Query Match 86.0%; Score 1060; DB 2; Length 239;
 Best Local Similarity 85.4%; Pred. No. 2,9e-80;
 Matches 204; Conservative 18; Mismatches 15; Indels 2; Gaps 2;

QY 1 MCLPRL-VLMFWIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPRLGLMLMWPGSSGDVMTQSPVLTIGQPASISCRSTSLVSDGNTYLSW 60
 QY 60 YLQKQSPKLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLVGYTCFOGTAP 119
 DB 61 PQRRGQSPRLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLVGYTCFOGTAP 120
 QY 120 YTFGGGTLEIK-TAAAPSVFIIPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 178
 DB 121 STFGGTLEIKRTVAAPSVFIIPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 180
 QY 179 SGNSESVTEODSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTSFNRGEC 237
 DB 181 SGNSESVTEODSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTSFNRGEC 239

RESULT 2
 Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
 ID Q6P491_HUMAN PRELIMINARY; PRT; 239 AA.
 AC Q6P491;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 OS Hypothetical protein.
 OC Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE-Skin;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stacieleon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Mizny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield V.S.N., Krzywinski M.I., Skalske M., Smalhus D.B.,
 RA Schermer A., Schein J.E., Jones S.J.W., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE-Skin;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC063599; AAH63599.1; -, mRNA.
 DR HSSP, P01837; 1KCU.
 DR SMR, Q6P491; 21-237.
 DR InterPro, IPR003599; IG.
 DR InterPro, IPR007110; IG-like.
 DR InterPro, IPR003597; IG-cl.
 DR InterPro, IPR003006; IG_MHC.
 DR InterPro, IPR003596; IG_v.
 DR Pfam, PF07654; Cl-set; 1.
 DR SMART, SM00409; IG; 2.
 DR SMART, SM00407; IGV; 1.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG_LIKE; 2.
 DR PROSITE, PS50290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26245 MW; CD7313DDPFD358B3 CRC64;

Query Match 84.8%; Score 1045; DB 2; Length 239;
 Best Local Similarity 83.7%; Pred. No. 5,3e-79;
 Matches 200; Conservative 19; Mismatches 18; Indels 2; Gaps 2;

QY 1 MCLPRL-VLMFWIPASSDYLMTQTPLSLVISGDOASISCRSSQTIHNSGNTYLEM 59
 DB 1 MCLPRLGLMLMWPGSSGDVMTQTPLSVLTIGQPASISCRSSSLHSNGNTYLSW 60
 QY 60 YLQKQSPKLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLVGYTCFOGTAP 119
 DB 61 LHQRPQSPRLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEADLVGYTCFOGTAP 120
 QY 120 YTFGGGTLEIK-TAAAPSVFIIPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 178
 DB 121 RTFGGTVEIKRTVAAPSVFIIPPSDQLKSGTASVCLNNFYPREAKVQMKYDNLQ 180
 QY 179 SGNSESVTEODSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTSFNRGEC 237
 DB 181 SGNSESVTEODSKSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTSFNRGEC 239

RESULT 3
 Q8N8KO_HUMAN PRELIMINARY; PRT; 239 AA.
 ID Q8N8KO_HUMAN PRELIMINARY; PRT; 239 AA.
 AC Q8N8KO;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 OS IGV1-5 protein.
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Prostate;
 RA Director MGC Project;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=1601042;
 RA Huber C., Klobbeck H.G., Zachau H.G.;
 RT "Ongoing V kappa-J kappa recombination after formation of a productive
 V kappa-J kappa coding joint.";
 RL Eur. J. Immunol. 22:1561-1565 (1992).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8436174;
 RA Wagner S.D., Luzzatto L.;
 RT "V kappa gene segments rearranged in chronic lymphocytic leukemia are
 distributed over a large portion of the V kappa locus and do not show
 somatic mutation.";
 RL Eur. J. Immunol. 23:391-397 (1993).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=8258341;
 RA Klein R., Jaenichen R., Zachau H.G.;
 RT "Expressed human immunoglobulin kappa genes and their hypermutation.";
 RL Eur. J. Immunol. 23:3248-3262 (1993).
 DR EMBL: BC030814; AAH30814.1; -, mRNA.
 DR PIR: S23638; S23638.
 DR PIR: S34091; S34091.
 DR PIR: S40342; S40342.
 DR PIR: S40357; S40357.
 DR HSSP: P01834; 117Z.
 DR SMR: Q8NEK0; 21-237.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF07654; C1-sect; 1.
 DR SMART: SM00406; IGV, 1.
 DR PROSITE: PS00835; IG_LIKE; 2.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 DR Immunoglobulin domain.
 SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 83.8%; Score 1032; DB 2; Length 239;
 Best Local Similarity 82.8%; Pred. No. 6-4e-78;
 Matches 198; Conservative 19; Mismatches 20; Indels 2; Gaps 2;
 QY 1 MCLPVRLI-VIMFIMPASSDVLMTQPLSLPVSIGDQASISCRSSQITVHSNGNTYLEW 59
 DB 1 MRPLQGLGLMLWVSGSSGDIWMTQSPISLPVTFGEPAISICRSSQGLHSDGYNVLDW 60
 QY 60 YLQKRGQSPKLLIKVSRPFGVDPFRFGSGSGDFTLKISRVKVEDIGVYCFQGTAP 119
 DB 61 YLQKRGQSPKLLIKVSRPFGVDPFRFGSGSGDFTLKISRVKVEDIGVYCFQGTAP 120
 QY 120 YTFGGGTLELRK-TAAPSVFIFPPSDDQLKSGTAVVCLINFFYPRAKYQMKYDNLQ 178
 DB 121 QTFGGGTLELRKTAAPSVFIFPPSDDQLKSGTAVVCLINFFYPRAKYQMKYDNLQ 180
 QY 179 SGNQSESVTEODSKDSTYSLSTLTLSADYDKKRVACEVTHQGLSSPVTKSFNRGEC 237
 DB 181 SGNQSESVTEODSKDSTYSLSTLTLSADYDKKRVACEVTHQGLSSPVTKSFNRGEC 239
 RESULT 4
 Q6PIH6 HUMAN PRELIMINARY; PRT; 240 AA.
 ID Q6PIH6;
 AC Q6PIH6;
 DT 05-JUN-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE IGKV1-5 protein.
 GN Name=IGKV1-5;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Cavaletto T.L., Scheetz T.E.,
 RA Brownstein M.J., Ussell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RA Director MGC Project;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC034142; AAH34142.1; -, mRNA.
 DR HSSP: P01837; 1KB5.
 DR SMR: Q6PIH6; 23-240.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_v.


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RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Straube R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -, mRNA.
DR SRR; O6GMV9; 21-235.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 73.9%; Score 911; DB 2; Length 235;
Best Local Similarity 73.2%; Pred. No. 7.9e-68;
Matches 175; Conservative 32; Mismatches 26; Indels 6; Gaps 3;

QY 1 MKLPVRL-VLMFWIPASSDVMTQTPLSLPVSLGDQASISCRSSQTIIVHSNGTYLFW 59
DB 1 METPAQLFLFLLLMLPDTGTGEIVLTQSPGTLSLSPGERAALSCRASQSV---NKKYLAW 56

QY 60 YLQKRGQSPKLLIYKVSNRSPGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTAA 119
DB 57 YQKRGQAPRLIMYASIRATGIPDRFSGSGSGTDFTLTIRLEEDAVAVFCQGYGSP 116

QY 120 YTFGGGTGLKLR-TAAPSVPFIPPPSDQKSGTASVVCLLNFFYPREAVQWQVDNAL 178
DB 117 LTFGGGTGLKLR-TAAPSVPFIPPPSDQKSGTASVVCLLNFFYPREAVQWQVDNAL 176

QY 179 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 177 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 235

RESULT 7
O6P5S8_HUMAN PRELIMINARY; PRT; 236 AA.
ID O6P5S8_HUMAN PRELIMINARY; PRT; 236 AA.
AC O6P5S8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Scheefel C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;
RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.;
RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carinci P.; Prange C.;
RA Raha S.S.; Loguella N.A.; Peters G.J.; Abramson R.D.; Mullaly S.J.;
RA Boeck S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gutarra P.H.;
RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;
RA Villalón D.K.; Wozny K.C.; Sodergren E.J.; Lu X.; Gibbs R.A.;
RA Fahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.;
RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

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RA Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;
RA Rodriguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;
RA Butlerfield Y.S.N.; Krzywinski M.I.; Skalska U.; Small D.E.;
RA Schnerch A.; Schein J.E.; Jones S.J.M.; Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Glandular pool- thyroid;
RA Straube R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -, mRNA.
DR HSSP; P01837; 1KCU.
DR SRR; O6P5S8; 21-236.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 73.7%; Score 907.5; DB 2; Length 236;
Best Local Similarity 73.3%; Pred. No. 1.5e-67;
Matches 176; Conservative 31; Mismatches 26; Indels 7; Gaps 4;

QY 1 MKLPVRL-VLMFWIPASSDVMTQTPLSLPVSLGDQASISCRSSQTIIVHSNGTYLFW 59
DB 1 METPAQLFLFLLLMLPDTGTGEIVLTQSPGTLSLSPGERATLSCRASQTFSS---HLAW 56

QY 60 YLQKRGQSPKLLIYKVSNRSPGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTAA 118
DB 57 YQKRGQAPRLIMYASIRATGIPDRFSGSGSGTDFTLTIRLEEDAVAVFCQGYGSP 116

QY 119 PYTFGGGTGLKLR-TAAPSVPFIPPPSDQKSGTASVVCLLNFFYPREAVQWQVDNAL 177
DB 117 SLTFGGGTGLKLR-TAAPSVPFIPPPSDQKSGTASVVCLLNFFYPREAVQWQVDNAL 176

QY 178 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 237
DB 177 QSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 236

RESULT 8
O6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
ID O6GMX8_HUMAN PRELIMINARY; PRT; 236 AA.
AC O6GMX8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE IGKC protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.;
RA Klausner R.D.; Collins F.S.; Wagner L.; Shemen C.M.; Schuler G.D.;
RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Scheefel C.F.; Bhat N.K.;
RA Hopkins R.F.; Jordan H.; Moore T.; Max S.I.; Wang J.; Hsieh F.;
RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.;

```

RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-cells;
 RG NIH MCC Project;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073764; AAH73764.1; -; mRNA.
 DR SMR; O6GMX8; 24-235.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR SEQUENCE 236 AA; 25707 MW; 4FCBRL4B559EFC9 CRC64;
 60
 Query Match 73.2%; Score 901.5; DB 2; Length 236;
 Best Local Similarity 73.6%; Pred. No. 4,9e-67;
 Matches 176; Conservative 24; Mismatches 32; Indels 7; Gaps 3;
 1 MCLPVRLL-VLMFWIPASSSDVLTMTOTPLSLPVLGDDQASISCRSQTIVHNGNTYLEM 59
 Db 3 MGVPAQLLFLLLMFLPFSGRCIDTOMTOSPSVASVSDRTVITCRASQGI-----SSALW 57
 QY 60 YLQKPGQSPKLLIYKVSINRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFOGTNAP 119
 Db 58 YQKKGQAPKRLIYAASISLGVPSPFSGSGSGTDFTLTSLQPEDFAVYYCCQAHSPF 117
 QY 120 YTFGGGTGLEIK-TAAAPSVFTFPSPDEQLKSGTASVCLNNFYPREAKVOMKVDNALQ 178
 Db 118 FTFGPGTKVDIKRTVAAPSVFTFPSPDEQLKSGTASVCLNNFYPREAKVOMKVDNALQ 177
 QY 179 SGNDSQSVTEODSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSVYTSFNRGEC 237
 Db 178 SGNDSQSVTEODSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSVYTSFNRGEC 236
 RESULT 9
 O6PJP2 HUMAN PRELIMINARY; PRT; 235 AA.
 AC O6PJP2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 OS Hypothetical protein.
 OC Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lung;
 RG Strusberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016380; AAH16380.1; -; mRNA.
 DR HSSP; P01837; 1KCU.
 DR SMR; O6PJP2; 21-235.
 DR Ensembl; ENSG00000163245; Homo sapiens.
 DR InterPro; IPR003599; IG_1.
 DR InterPro; IPR007110; IG_1like.
 DR InterPro; IPR003597; IG_1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG1; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 DR SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;
 60
 Query Match 73.1%; Score 900; DB 2; Length 235;
 Best Local Similarity 72.4%; Pred. No. 6,5e-67;
 Matches 173; Conservative 32; Mismatches 28; Indels 6; Gaps 3;
 1 MCLPVRLL-VLMFWIPASSSDVLTMTOTPLSLPVLGDDQASISCRSQTIVHNGNTYLEM 59
 Db 1 MGVPAQLLFLLLMFLPFSGRCIDTOMTOSPSVASVSDRTVITCRASQGI-----SSALW 56
 QY 60 YLQKPGQSPKLLIYKVSINRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFOGTNAP 119
 Db 57 YQKKGQAPKRLIYAFSSSRATGIPDRFSGSGSGTDFTLTSLQPEDFAVYYCCQYGSQ 116
 QY 120 YTFGGGTGLEIK-TAAAPSVFTFPSPDEQLKSGTASVCLNNFYPREAKVOMKVDNALQ 178
 Db 117 FTFGPGTKVDIKRTVAAPSVFTFPSPDEQLKSGTASVCLNNFYPREAKVOMKVDNALQ 176
 QY 179 SGNDSQSVTEODSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSVYTSFNRGEC 237
 Db 177 SGNDSQSVTEODSKOSTYSLSTLTLSKADYKHKVYACEVTHQGLSSVYTSFNRGEC 235
 RESULT 10
 O6GMN1 HUMAN PRELIMINARY; PRT; 236 AA.
 AC O6GMN1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 OS IGKC protein.
 GN Name=IGKC;

Query Match	72.8%; Score 896.5; DB 2; Length 236;
Best Local Similarity	73.6%; Pred. No. 1.3e-66;
Matches 176;	Conservative 23; Mismatches 33; Indels 7; Gaps 3
OY	1 MCLPYRLI-VIMFWIPASSSDVLTOTPLISLPLSLGDAQASISCRSSQTIHNSGNTTYLW 59
DB	3 MRVPALLGILLMLTPGARCALIQMTQSPSSLASVGDRTVITICRASQGISINDLG-----W 57
OY	60 YLQKRGSGPKLITYKVSNRFGVDPDRFGSSGSGCTPFLTKISVVEABDLGVVYCPQGTAP 119
DB	58 YQKRGKAPKLITYAASSLQSGSVNPFSSGSGCTPFLTSLSLPDPFATVYCLDQYNP 117
OY	120 YTFGGGTGLKLEIK-TAAAPSVFIFPPSDDEQLKSGTASVVCILANFPYPRKAYQMKYDNLQ 178
DB	118 WTFGGGTVEIKRTYTAAPSVFIFPPSDDEQLKSGTASVVCILANFPYPRKAYQMKYDNLQ 177
OY	179 SGNSESATBEDSKDSTSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 237
DB	178 SGNSESATBEDSKDSTSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 236

1D O6GMXO HUMAN PRELIMINARY; PRT; 236 AA.

AC

DB 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

CC Homo.

OX NCBI_TaxID=9606;

XP [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Splice.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Fergold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H.B., Moore T., Max S.I., Wang J., Hsieh F.,

RA Ditschenko L., Marziani K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.P., Casavant T.J., Scheetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gundrathe P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

RA Schermer A., Schein J.B., Jones S.J.M., Matra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP [2]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Splice;

RL Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC073775; AAH73775.1; -; mRNA.

DR SMR; O6GMXO; 23-236

DR GO; GO:0016021; C:integral to membrane; IEA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_V.

DR Pfam; PF07654; CI-bec; I.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IG; 1.

DR PROSITE; PS00835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

DR Hypothetical protein.

KW SEQUENCE 236 AA; 25807 MW; 864EA08C7E92B8F CRC64;

SO

Query Match 72.6%; Score 894.5; DB 2; Length 236;

Best local similarity 73.2%; Pred. No. 1.9e-66;

Matches 175; Conservative 21; Mismatches 36; Indels 7; Gaps 3;

QY 1 MCLPVRLL-VLMFWIPASSSDVLTMTQPLSLVSLGDAQISCRSSQTIYHSNGNTYLEW 59

DB 3 MRVPAQLLGLLLMLRGARCDIQMTQSPSSLSASGVGRVITCRASQNI-----NNYLNW 57

QY 60 YLQRPQGSFKLLTYKVSRRFSGVDPRSGSGSGDDFTLTKTSRVVAEDLGVVYVYCFQGTAP 119

DB 58 YQLRGRKAPMLLITAAASLQSGVSRSGSGSGTDFLTLLTSSLRPDDPATRYVCOOSYVIP 117

QY 120 YTPGGGTLEIK-TAAAPSVTIPPPSPDQLSGTASVVCCLINNFYPREAKYQMKVDNALQ 178

DB 118 LTFGGGTVETIKRTVAAPSVITFPSPDQLSGTASVVCCLINNFYPREAKYQMKVDNALQ 177

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Qy 179 SGNQSEVTEBQSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 237
Db 178 SGNQSEVTEBQSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 236

RESULT 12
O6P1H7 HUMAN PRELIMINARY; PRT; 236 AA.
ID O6P1H7
AC O6P1H7
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RG NIH MGC Project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC034141; AAH34141.1; -; mRNA.
DR HSSP: P01607; IAR2.
DR SMR: P01607; 23-236.
DR Ensemble: ENSG00000163245; Homo sapiens.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003066; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG_C1; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25603 MW; 8BC66110661213F CRC64;

Query Match 72.5%; Score 893.5; DB 2; Length 236;
Best Local Similarity 73.2%; Pred. No. 2,3e-66;
Matches 175; Conservative 24; Mismatches 33; Indels 7; Gaps 3;

1 MKLPVRLT-VLMFWIPASSSDVMTQTPSLPLVSLDQASISCRSQTIVHSNGNTYLEM 59
3 MNPVSQLGLLMLPLFACACDIOITQSPSPFLASVDRVYITICRASQGI-----SSYLEM 57

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Qy 60 YLQKQSPKLLIYVNSRFGVDPDRFGSGSGDFTLKISRVNEDLCVYFCQGTAP 119
Db 58 YQKPKAPNLLIYVNSRFGVDPDRFGSGSGDFTLTLSLQPEDATVYCCQQLNSP 117

120 YTPGGGTLEIK-TAAPSVPFIPPSDQLSGTASVYCLANNFYPREAKVOMKDNALQ 178
118 PTFGGGIVEIKRTYAAPSVFIPPSDQLSGTASVYCLANNFYPREAKVOMKDNALQ 177

Qy 179 SGNQSEVTEBQSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 237
Db 178 SGNQSEVTEBQSKDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTYSFNRGEC 236

RESULT 13
O6GMW0 HUMAN PRELIMINARY; PRT; 235 AA.
ID O6GMW0
AC O6GMW0
DT 05-JUL-2004 (TRMBLrel. 27, Created)
DT 05-JUL-2004 (TRMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRMBLrel. 27, Last annotation update)
DE IGKV1-5 protein.
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC073792; AAH73792.1; -; mRNA.
DR SMR: O6GMW0; 21-233.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG_1like.
DR InterPro: IPR003597; IG_C1.
DR InterPro: IPR003066; IG_MHC.
DR InterPro: IPR003596; IG_V.
DR Pfam: PF07654; C1-set; 1.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IG_C1; 1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS50835; IG_LIKE; 2.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.4%; Score 892; DB 2; Length 235;

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Best Local Similarity 73.8%; Pred. No. 3e-66;
Matches 177; Conservative 28; Mismatches 27; Indels 8; Gaps 5;

QY 1 MKLPRLL-VLMFPIPASSDVLMTQTPLSLPVSLGDDASISCRSSQTIHNSNGTYLEW 59
Db 1 MEAPQQLFLFLLLMLPDSITGEIVMTQSPATLSVSPGERATLSCRASQSI--SNN---LAW 55
QY 60 YLQKPGSPKLLIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDGYYVCFQGTAA 118
Db 56 YQKRGKAPQLLIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDGYYVCFQGTAA 115
QY 119 PYTFGGGTLEIK-TAAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKYQWKVDNL 177
Db 116 LYTPEGGKTKLEIKRTVAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKYQWKVDNL 175
QY 178 SGNQSESVTEBDSKDSITSLSTLTLSKADYEKKKVAACEVTHQGLSSPYTKSFNRGEC 237
Db 176 SGNQSESVTEBDSKDSITSLSTLTLSKADYEKKKVAACEVTHQGLSSPYTKSFNRGEC 235

RESULT 14

Q72473_HUMAN PRELIMINARY; PRT; 234 AA.
AC Q72473;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=lung;
RG NIH MGC Project;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAHS6256.1; -; mRNA.
DR HSSP; P01834; 1HEZ.
DR SMR; Q72473; 22-234.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003557; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-sect; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Immunoglobulin domain.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 71.8%; Score 884.5; DB 2; Length 234;
Best Local Similarity 72.8%; Pred. No. 1.3e-65;
Matches 174; Conservative 23; Mismatches 35; Indels 7; Gaps 3;

QY 1 MKLPRLL-VLMFPIPASSDVLMTQTPLSLPVSLGDDASISCRSSQTIHNSNGTYLEW 59
Db 1 MRVPAQLGLLLMLPGARCAIRMTQSPSPASGDRVTTCRASQSI-----GSYLAW 55
QY 60 YLQKPGSPKLLIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDGYYVCFQGTAA 119
Db 56 YQKRGKAPQLLIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDGYYVCFQGTAA 115
QY 120 YTFGGGTLEIK-TAAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKYQWKVDNL 178
Db 116 WTFGGGTLEIKRTVAAPSVFIPPPSDQLKSGTASVVCCLNNFYPREAKYQWKVDNL 175
QY 179 SGNQSESVTEBDSKDSITSLSTLTLSKADYEKKKVAACEVTHQGLSSPYTKSFNRGEC 237
Db 176 SGNQSESVTEBDSKDSITSLSTLTLSKADYEKKKVAACEVTHQGLSSPYTKSFNRGEC 234

RESULT 15

Q502W4_HUMAN PRELIMINARY; PRT; 236 AA.
AC Q502W4;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE IGKC protein.
GN Name=IGKC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.B.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=glandular pool- thyroid;
RG NIH MGC Project;
RL Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC095489; AAHS9489.1; -; mRNA.
DR SMR; Q502W4; 23-236.
DR Ensembl; ENSG00000163245; Homo sapiens.
DR InterPro; IPR003599; Ig.

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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:45:30 ; Search time 32.3863 Seconds
(without alignments)
1372.562 Million cell updates/sec

Title: US-10-828-782A-18

Perfect score: 2490
Sequence: 1 MESSCVMLFLSLGTAGVLSF.....MREALHNRYTQKSLSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1755	70.5	326	1 G2HU	Ig gamma-2 chain C
2	1605.5	64.5	327	1 G4HU	Ig gamma-4 chain C
3	1604	64.4	330	1 G4HU	Ig gamma-4 chain C
4	1599.5	64.2	469	2 S37483	Ig gamma-2a chain C
5	1578.5	63.4	377	2 A23511	Ig gamma-3 chain C
6	1569.5	63.0	377	2 A60764	Ig gamma-3 chain C
7	1549	62.2	446	2 S40295	Ig gamma-2a chain C
8	1545	62.0	474	1 G4MS11	Ig gamma-2b chain C
9	1490.5	59.9	475	2 S01321	Ig gamma-2b chain C
10	1481	59.5	470	2 S20800	Ig heavy chain pre
11	1465	58.8	472	2 S31459	Ig gamma-1 chain-
12	1430.5	57.4	444	2 PC4436	monoclonal antiod-
13	1316	52.9	374	2 S69339	Ig heavy chain V r
14	1271	51.0	328	2 I47159	Ig gamma 2a chain
15	1265	50.8	328	2 I47160	Ig gamma 2b chain
16	1246	50.0	328	2 I47161	Ig gamma 3 chain C
17	1236	49.6	328	2 I47158	Ig gamma 1 chain C
18	1207.5	48.5	323	1 G4HB	Ig gamma chain C r
19	1176.5	47.2	329	1 G2GP	Ig gamma-2 chain C
20	1164	46.7	326	1 P60017	Ig gamma-1 chain C
21	1151	46.2	255	4 S31866	Ig gamma-1 chain C
22	1145.5	46.0	308	2 C30554	Ig heavy chain C r
23	1143	45.9	324	1 G4MS	Ig gamma-1 chain C
24	1138	45.7	393	1 G4MSM	Ig gamma-1 chain C
25	1134	45.5	234	1 P70207	Ig gamma chain C r
26	1120.5	45.0	333	2 P60018	Ig gamma-2b chain
27	1120	45.0	322	2 P60019	Ig gamma-2a chain
28	1115.5	44.8	327	2 S06611	Ig gamma-2 chain C
29	1114	44.7	289	1 G3HWT	Ig gamma-3 heavy c

30	1111.5	44.6	329	2 S00847	Ig gamma-2c chain
31	1097	44.1	329	1 G3MSC	Ig gamma-3 chain C
32	1095	44.0	330	1 G3MSA	Ig gamma-2a chain
33	1090	43.8	399	1 G3MSM	Ig gamma-2a chain
34	1086	43.6	398	1 G3MSM	Ig gamma-3 chain C
35	1083.5	43.5	335	1 G2MSAB	Ig gamma-2a chain
36	1068	42.9	277	2 I47162	Ig gamma 4 chain C
37	1054	42.3	405	1 G4MSBM	Ig gamma-2b chain C
38	943	37.9	548	2 S38864	Ig epsilon chain C
39	937.5	37.7	241	2 S69131	Ig heavy chain (DO
40	892.5	35.8	549	2 S04845	Ig heavy chain pre
41	857	34.4	246	2 S38950	Ig gamma chain - m
42	829	33.3	627	2 S14683	Ig mu chain precu
43	758.5	30.5	572	2 B46529	Ig y heavy chain (
44	725	29.1	220	2 A49444	Ig gamma-1 heavy c
45	721.5	29.0	249	2 S69340	Ig heavy chain VH1

ALIGNMENTS

RESULT 1

G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text_change 09-Jul-2004
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Bliss, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain cor
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <RLL>
A:Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFC; GB:V00554; GB:J00230; NID:932
A>Note: Lys-326 is probably removed posttranslationally
A:Name: Lys-326; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A:Cross-references: UNIPARC:UPI0000173791
A>Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:8001357; PMID:113060
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A:Cross-references: UNIPARC:UPI0000173792; UNIPARC:UPI0000173793
A>Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
A:Cross-references: UNIPARC:UPI0000173794
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A>Note: the revised sequence differs from that shown in having 60-Ala and in the amidati
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971

A>Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500; PMID:4940472
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R/Fingstone, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124; PMID:5782707
A/Contents: annotation; Sa, disulfide bonds
C/Genetics:
A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/133-202/Domain: immunoglobulin homology <IM1>
F/1239-306/Domain: immunoglobulin homology <IM2>
F/124/Dsulfide bonds: interchain (to light chain) #status experimental
F/127-83.140-200.246-304/Dsulfide bonds: #status experimental
F/102.103.106.109/Dsulfide bonds: interchain (to heavy chain) #status experimental
F/176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 70.5%; Score 1755; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 1.9e-94;
Matches 326; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 137 ASTGSPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 196
DB 1 ASTGSPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
QY 197 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKVERKCCVCPCPAPPPVAGPSVF 256
DB 61 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKVERKCCVCPCPAPPPVAGPSVF 120
QY 257 LFPPPKPDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGVENAKTKPREEQFNSTFR 316
DB 121 LFPPPKPDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGVENAKTKPREEQFNSTFR 180
QY 317 VSVSLTVVHODMLNGEKYCKVSNKGDLPAPIEKTIISKTKGQPREPOVYTLPPSRREMTKN 376
DB 181 VSVSLTVVHODMLNGEKYCKVSNKGDLPAPIEKTIISKTKGQPREPOVYTLPPSRREMTKN 240
QY 377 QVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSEFLYSKLTVDKSRWQOG 436
DB 241 QVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSEFLYSKLTVDKSRWQOG 300
QY 437 VFSCSVMEHALHNHYTKSLISLSPGK 462
DB 301 VFSCSVMEHALHNHYTKSLISLSPGK 326
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RESULT 2

GHNU
Ig gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004
A/Accession: A90933; MUID:83157104; PMID:6299662
A/Molecule type: DNA
A/Residues: 1-327 <ELU>
A/Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A/Note: The sequence was determined from the germline gene
R/Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A>Title: Human immunoglobulin sublcasses. Partial amino acid sequence of the constant
A/Accession: A90249; MUID:70207560; PMID:4192699

A/Molecule type: protein
A/Residues: 1-30/81-326 <PIN>
A/Cross-references: UNIPARC:UPI0000173795; UNIPARC:UPI0000173796
C/Genetics:
A/Gene: GDB:IGHG4
A/Cross-references: GDB:119340; OMIM:147130
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1; 111/1; 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F/20-85/Domain: immunoglobulin homology <IM1>
F/99-110/Region: hinge
F/134-203/Domain: immunoglobulin homology <IM2>
F/1240-307/Domain: immunoglobulin homology <IM3>
F/14/Dsulfide bonds: interchain (to light chain) #status experimental
F/127-83.141-201.247-305/Dsulfide bonds: #status predicted
F/106.109/Dsulfide bonds: interchain (to heavy chain) #status experimental
F/177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.5%; Score 1605.5; DB 1; Length 327;
Best Local Similarity 92.4%; Pred. No. 7.9e-86;
Matches 302; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

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QY 137 ASTGSPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 196
DB 1 ASTGSPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSS 60
QY 197 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKVERKCCVCPCPAPPPVAGPSVF 255
DB 61 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKVERKCCVCPCPAPPPVAGPSVF 120
QY 256 LFPPPKPDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGVENAKTKPREEQFNSTFR 315
DB 121 LFPPPKPDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGVENAKTKPREEQFNSTFR 180
QY 316 RVSVSLTVVHODMLNGEKYCKVSNKGDLPAPIEKTIISKTKGQPREPOVYTLPPSRREMTKN 375
DB 181 RVSVSLTVVHODMLNGEKYCKVSNKGDLPAPIEKTIISKTKGQPREPOVYTLPPSRREMTKN 240
QY 376 NOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSEFLYSKLTVDKSRWQOG 435
DB 241 NOVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPMLDSGSEFLYSKLTVDKSRWQOG 300
QY 436 VFSCSVMEHALHNHYTKSLISLSPGK 462
DB 301 VFSCSVMEHALHNHYTKSLISLSPGK 327
```

RESULT 3

GHNU
Ig gamma-1 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text_change 09-Jul-2004
A/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R/Elleston, J.W.; Bereson, B.J.; Hood, L.B.
Nucleic Acids Res. 10, 4071-4079, 1982
A>Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A/Reference number: A93433; MUID:82274238; PMID:6287432
A/Accession: A93433
A/Molecule type: DNA
A/Residues: 1-330 <ELU>
A/Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0B; EMBL:Z17370
A/Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers,
R/Harris, L.J.
submitted to the EMBL Data Library, October 1992
A/Reference number: S33904
A/Accession: S36861
A/Molecule type: DNA
A/Residues: 2-330 <HAR>
A/Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370

R.Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Homjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:811133
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113,235-330 <TAK>
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:217370
R.Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Wexdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. VII. Amino acid sequen
A:Reference number: A50563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: Protein
A:Residues: 1-96,'R',98-135 <CUN>
A:Cross-references: UNIPARC:UPI000017378D
A:Note: this sequence has the Gm(3) marker, 97-Arg
R.Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. VII. Amino acid sequen
A:Reference number: A50564; MUID:71064025; PMID:5530842
A:Contents: Eu
A:Accession: A90564
A:Molecule type: Protein
A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A:Cross-references: UNIPARC:UPI000017378E
A:Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met
R.Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
Igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: Protein
A:Residues: 1-94,'Q',36-96,'R',98-115,'Q',117-197,'D',199-238,'D',240,'E',242-268,'E',27
A:Cross-references: UNIPARC:UPI000017378F
A:Note: this sequence has the Gm(17) and Gm(1) markers
R.Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131; PMID:684994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: Protein
A:Residues: 1-96,'R',98-197,'D',199-238,'E',240,'W',242-266,'D',268-271,'D',273-330 <SCH
A:Cross-references: UNIPARC:UPI0000173790
A:Note: this sequence has the Gm(3) and Gm(non-1) markers
R.Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammae-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R.Draker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
endosome cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
A:Accession: A91667
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental

F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 64.4%; Score 1604; DB 1; Length 330;
Best Local Similarity 91.2%; Pred. No. 9.8e-86;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;
QY 137 ASTKPSVFPLAPSPRSSTSESTALGCLVQYFPEPVVSNMGSALTSGVHTFPAVLQSS 196
DB 1 ASTKPSVFPLAPSPRSKSTSGSTALGCLVQYFPEPVVSNMGSALTSGVHTFPAVLQSS 60
QY 197 GLYSLSVTVTPSSNFGTQYTCNVDRKPSNTKYDKYVERKCYE--CPGPCPP-VAG 252
DB 61 GLYSLSVTVTPSSSLGTQYTCNVNHRPSNTKYDKYVERKCYE--CPGPCPP-VAG 120
QY 253 PSYVLPFPKPDITMISTPTEVTCVVDVSHEDRQVPMVVDGVENVNATKPREEPN 312
DB 121 PSYVLPFPKPDITMISTPTEVTCVVDVSHEDRQVPMVVDGVENVNATKPREEQYN 180
QY 313 STPRVSVLTVVHDPMVNGEKYCKVSNKGPAPRIEKTISKTKQPREQYVTLPPSRER 372
DB 181 STPRVSVLTVVHDPMVNGEKYCKVSNKGPAPRIEKTISKTKQPREQYVTLPPSRER 240
QY 373 MTKNQVSLTCLVKGFYPSDIAVEESNQPENNYKTTPMLDSDGFFYSKLTVDKSRW 432
DB 241 LTKNQVSLTCLVKGFYPSDIAVEESNQPENNYKTTPMLDSDGFFYSKLTVDKSRW 300
QY 433 QCGVFSGVSWHKEALHNTYTKSISLSPGK 462
DB 301 QCGVFSGVSWHKEALHNTYTKSISLSPGK 330

RESULT 4

S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R.Ducancel, F.P.D.
Submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: UNIPARC:UPI00002PB47; EMBL:X70423; MUD:9406252; PIDN:CAA49868.1; PI
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 64.2%; Score 1599.5; DB 2; Length 469;
Best Local Similarity 65.1%; Pred. No. 2.6e-85;
Matches 306; Conservative 60; Mismatches 95; Indels 9; Gaps 5;
QY 1 MECSVWMLFLISAGVTLSEVLOQSGPELVKPGASVMSKASGYTDDYIHMMKQSH 60
DB 1 MGSMTFLFLISAGVTHCQQLQDQSGPELVKPGASVMSKASGYTDDYIIMVKKXP 60
QY 61 GKSLEWIGYIYPNNGNGYNOKFGKATLTVDKSSSTAYMELRTLTSDSAIVYCGR-- 117
DB 61 GQGLKMGWIIYPAGNTRKYNENFKGKATLTVDSSSTAYMGLSLSSTSDTAIVYFCARLNG 120
QY 118 STMDPFDYWGCGTTLTYSASATKPSVPLAPCSRSTSESTALGCLVQYFPEPVTVSW 177
DB 121 ATATLLDWGGGTLTVSSACTTAPSVPLAPVCGDTTGGSSVTLCGLVGFPEPVTLTW 180
QY 178 NSGALTSGVHTFPAVLQSSGLYSLSVTVTPSSNFGTQYTCNVDRKPSNTKYDKYVERK 237
DB 181 NSGALTSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQITCNVAHPASSTKVDKXIPR 239
QY 238 --CCVCECP--CPAPP-VAGPSVLPFPKPDITMISTPTEVTCVVDVSHEDRQVPMV 292

F:231-340/Domain: C2 region <CH3>
 F:341-446/Domain: C3 region <CH3>
 F:360-427/Domain: immunoglobulin homology <IM1>
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:12-96,144-159,261-321,367-425/Disulfide bonds: #status predicted
 F:133/Disulfide bonds: interchain (to light chain) #status predicted
 F:224,227,229/Disulfide bonds: interchain #status predicted
 F:297/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 62.2%; Score 1549; DB 2; Length 446;
 Best Local Similarity 65.3%; Pred. No. 2e-82;
 Matches 292; Conservative 58; Mismatches 91; Indels 6; Gaps 4;

QY 20 EVLOQSGPELVKPPASVYMSKASGYGTDYIIHMQSHKSLWIIYIYNNKNGY 79
 DB 1 QILOQSGPELVKPPASVYMSKASGYGTDYIIHMQSHKSLWIIYIYNNKNGY 60
 QY 80 NQKFKKATLVYDKSSSTAYMELRTLSSESAVYCGSTWDDPDYWGQSTLVSSAST 139
 DB 61 NEKFKGKATLVDTSSSTAYVQSLTSEDSAVYFCAGGKPAAMDYWGQSTLVSSAKT 120
 QY 140 KQPSVPLAPGCRSTSESTALGCLVQYFPEPVVSNMGSALTGCTFPVAVLOSSGLY 199
 DB 121 TAPSVYPLAPVCGDTGSSVTLGCLVQYFPEPVVTLNWSGSLSSGVHTFPVAVLOSSD-LY 179
 QY 200 SLSSVYVTPSSNFGQYOTGVNDHKNPNTKVDKTERK--CCVECP--CPAP--VAGPS 254
 DB 180 TLSSSVYVTPSSNFGQYOTGVNDHKNPNTKVDKTERK--CCVECP--CPAP--VAGPS 239
 QY 255 VFLPPEKPDVTLMSRTPEVTCVVDVSHEDPEVDFNNVVDGVEVNAATKPKREQFNST 314
 DB 240 VFIFPPKIKDVLMSLSPVTCVVDVSHEDPEVDFNNVVDGVEVNAATKPKREQFNST 299
 QY 315 FRVSVVLTVVHODVNGKSKYKCKVSNKGLPAPIEKTISTKQCPPEPVYTLPSREBMT 374
 DB 300 LRVVSLALPIQHDVMSGKFKCKVSNKGLPAPIEKTISTKQCPPEPVYTLPSREBMT 359
 QY 375 KNOVSLTCLVNGFYSDIADVEWESNGEPNNKTPPMIDSGSPVLSKLTVDSDRMQ 434
 DB 360 KKQVTLTVNDVDFMEDVIVENTNNGKTELVNKNTEPVLDSGSYFMSKLVKKVKNV 419
 QY 435 GNVFSCVWHEALHNHYTQKSLSLSPG 461
 DB 420 RNSVSCSVHBEGLNHNHTTKSRSRTPG 446

RESULT 8
 G2MS11
 Ig gamma-2b chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: S25057; A02157; A26235; A26233; A53598
 R:Fishcher, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.U.; Kreuzaler, F.
 submitted to the EMBL Data Library, July 1992
 A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neocorp specific m
 A:Reference number: S25057
 A:Accession: S25057
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-474 <FIS-
 A:Cross-references: UNIPROT: P01866; UNIPARC: UP10000116095; EMBL: X67210; NID: g54826; PIDN
 R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
 Nature 283, 786-789, 1980
 A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
 A:Reference number: A02157; MUID: 80120716; PMID: 6766534
 A:Contents: a allele
 A:Accession: A02157
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-474 <YAM>
 A:Cross-references: UNIPARC: UP1000027202; GB: J00461
 R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
 Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea
 A:Reference number: A26235; MUID: 80081501; PMID: 117548
 A:Contents: MPC 11
 A:Accession: A26235
 A:Molecule type: mRNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU1>
 A:Cross-references: UNIPARC: UP100001737AF
 A:Note: Lys-474 is probably removed posttranslationally
 R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
 Science 206, 1303-1306, 1979
 A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglo
 A:Reference number: A26232; MUID: 80081502; PMID: 117549
 A:Accession: A26232
 A:Molecule type: DNA
 A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU2>
 A:Cross-references: UNIPARC: UP100001737AF
 R:Ollo, R.; Rougeon, F.
 Nature 296, 761-763, 1982
 A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm
 A:Reference number: A26233; MUID: 82173203; PMID: 6803173
 A:Contents: b allele
 A:Accession: A26233
 A:Molecule type: DNA
 A:Residues: 138-161, 'L', 163-189, 'P', 193-300, 'R', 302-331, 'A', 333-437, 'D', 440-474 <OLI>
 A:Cross-references: UNIPARC: UP100001737B0; GB: J00461
 R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Iimura, T.; Takahash
 J. Biol. Chem. 269, 12345-12350, 1994
 A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
 A:Reference number: A53598; MUID: 94216359; PMID: 7512967
 A:Accession: A53598
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 234-251 <KIM>
 A:Cross-references: UNIPARC: UP100001737B1
 C:Comment: The a allele sequence is shown.
 C:Genetics:
 A:Introns: 138/1; 236/1; 258/1; 368/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: Immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
 F:157-222/Domain: immunoglobulin homology <IM1>
 F:236-257/Region: hinge
 F:281-350/Domain: immunoglobulin homology <IM2>
 F:387-454/Domain: immunoglobulin homology <IM3>
 F:152/Disulfide bonds: interchain (to light chain) #status predicted
 F:164-220,288-348,394-452/Disulfide bonds: #status predicted
 F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
 F:324/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 62.0%; Score 1545; DB 1; Length 474;
 Best Local Similarity 62.4%; Pred. No. 3.7e-82;
 Matches 296; Conservative 60; Mismatches 106; Indels 12; Gaps 4;

QY 1 MECSVWMLFLSGTGVLSVLOQSGPELVKPPASVYMSKASGYGTDYIIHMQSH 60
 DB 1 MEMSWIFFLSLGTRGVSEVLOQSGPELVKPPASVYMSKASGYGTDYIIHMQSH 60
 QY 61 GKSLEWIGYIYVNNNGNGYNOKFKGKATLVYDKSSSTAYMELRTLSSESAVYCGRS-T 119
 DB 61 GQGLEWIGYIYVNNNGNGYNOKFKGKATLVYDKSSSTAYMELRTLSSESAVYCGRS-T 120
 QY 120 WDDPEYWGQSTLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVVSNMS 179
 DB 121 YDFWYWGQSTLVYSSASTYKSPVPLAPGCRSTSESTALGCLVQYFPEPVVSNMS 180
 QY 180 GALTSGVTPVAVYVLOSGLYSLSSVYVTPSSNFGQYOTGVNDHKNPNTKVDKTEV---- 235
 DB 181 GSLSSVHTLQALLOSGLYSLSSVYVTPSSNFGQYOTGVNDHKNPNTKVDKTEV---- 240
 QY 236 ----RKC--CYECPCPAPV-AGPSVLPFPKPDVTLMSRTPEVTCVVDVSHEDPEV 288
 DB 241 ISTNCPCKCKCHKCPAPNLEGPSVIFPPNIDVLMISLTPVTCVVDVSHEDPEV 300

Qy	289	QPNMYVDSVEYHNNAKTKREQOFNSTFRVSVLTVYNQDMLANGKEYCKJNSNKLPAPIE	348
	:	:	:
Db	301	QISMFVNNVNBHTAQOTQHREDYNSITRIVSTLPIDHDMWSGKPKCKXNNKLLPSPIE	360
Qy	349	KTISKTKQPRBPVOYTLLPRSREEMTKNQVSLTCIYVGFGSDIAVEBMSGCPENNYKT	408
	:	:	:
Db	361	RTISKIKELVAPROYTILPPRAEQLSRDVSILTCLVWGFNGDISVEWTSGHTEBNYKD	420
Qy	409	TTPMLDDSGSFFLYSKLTVDKSRLMOQGNVFSQSVNHBALEHHHYOKSLSLSPGK	462
	:	:	:
Db	421	TAPVLDSSGSFFLYSKLMNKTSKWEKTDSEFCANVBHSBLKNAYTLKTTSRSPBK	474

RESULT 9

Ig gamma-2b chain precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Sep-1989 #sequence #revision 30-Sep-1989 #text_change 23-Jul-1999
 C:Accession: S01321
 C:Id:Waele, P.; Fiers, V.; van de Voorde, A.; Molemans, F.; Piers, W.
 C:J: J. Biochem. 176, 287-295, 1988
 A:Title: Expression in non-T lymphoid cells of mouse recombinant immunoglobulin directed against
 A:Reference number: S01320; PMID:88329081; PMID:3138116
 A:Accession: S01321
 A:Molecule type: mRNA
 A:Residues: 1-475 <DB1>
 A:Cross-references: UNIPARC:UPI0000115DDB; EMBL:X13168; NID:G51780; PIDN:CAA31580.1; PIR
 A:Note: This sequence was determined from the differentiated gene
 C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
 C:Keywords: Immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-475/Product: Ig gamma-2b chain #status predicted <MAT>
 F:159-223/Domain: immunoglobulin homology <IMM>

Query Match	59.9%	Score 1490.5	DB 2	Length 475
Best Local Similarity	60.7%	Pred. No. 5.2e-79		
Matches 289	Conservative	66	Mismatches 106	Indels 15
			Gaps	5

[illegible]

RESULT 10

S22080
Ig heavy chain precursor (B/MT 4A.17.H5.A5) - bovine
N/Alternate names: Ig gamma-1 chain C region (clone 8.10)
C/Species: Bos primigenius taurus (cattle)
C/Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S22080; S06610, A31303
R/Sanders, P.C.
Submitted to the EMBL Data Library, November 1991

A|Accession: 0220060
 A|Status: preliminary
 A|Molecule type: mRNA
 A|Residues: 1-870 <MAN>
 A|Cross-references: UNIPARC:UPI0000116007; EMBL:X62916; NID:9439; PIDD:CAA44699.1; PIDD:9439
 R|Synons, D.B.A.; Clarkson, C.A.; Beale, D.
 Mol. Immunol. 26, 841-850, 1989
 A|Title: Structure of bovine immunoglobulin constant heavy chain gamma 1 and gamma 2
 |Reference number: S06610; MUID:90097956; PMID:2513467

A:Accession: U00010
A:Molecule type: DNA
A:Residues: 142-470 <SYM>
A:Cross-references: UNIPARC:UPI0000176F36; EMBL:X16701
A>Note: the sequence was determined from the germline gene
C:Genetics:

A:introns: 25 or 5 amino acids
 C:superfamily: immunoglobulin C region; immunoglobulin homology
 C:keywords: glycoprotein, heterotetramer; immunoglobulin; membrane protein
 F:161-225/domain: immunoglobulin homology <IM>
 F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	59.5%;	Score 1481;	DB 2;	Length 470;
Best Local Similarity	60.0%;	Pred. No. 1.8e-78;		
Matches 281;	Conservative 65;	Mismatches 106;	Indels 16;	Gaps 6

[illegible]

RESULT 11

Ig gamma-1 chain - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 13-Jan-1995 #sequence revision 13-Jan-1995 #text change 16-Jul-1999

C:Accession: S31459
 R:Patel, S.; Nau, F.
 submitted to the EMBL Data Library, December 1992
 A:Reference number: S31459
 A:Accession: S31459
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-472 <PAT>
 A:Cross-references: UNIPARC:UPI0000176F35; EMBL:X69797
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 58.8%; Score 1465; DB 2; Length 472;
 Best Local Similarity 58.5%; Pred. No. 1.5e-77;
 Matches 278; Conservative 64; Mismatches 107; Indels 26; Gaps 5;

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QY 7 MFLISGAGVISEVOLQSGELVPGASVMSCKASGYGTDTYYIHMMKQSHKSLIEW 66
DB 5 LFLVLSAPRGVLSQVRLQBSGSLATLLQTLISVTCISGFSLNMYGVMDVROAPGKALEW 64
QY 67 IGYTPNNGNG-----YNQFKGKATLTVDKSSSTAYMEKRLTSEDSAVYYCGRSTW 120
DB 65 L-----GSGCYDEDIDYNPVLKGRSLSTYKDTSKSQVSLTSTVTBDAVYYCARVDY 117
QY 121 D-----DFPYMGQTTLTVSSASTKGPVPLAPCSRSTSESTALGCLVKQYFPP 172
DB 118 DSHAPAAVSYDFWPGGLISTLSASTPKYPLTSCCGDTSSIVTLGCLVSSYMEEP 177
QY 173 VTVSNAGALTSQVHTFPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDRKPSNTKVDK 232
DB 178 VTVNNSGALTSQVHTFPAVLQSSGLYSLSVTVTPASSGQTFICNVAPASSTKVDK 237
QY 233 TVERKCCVCEPCPPAP--VAGSVFLFPPPKXTTLMISRPETVCVVVDVSHDEPVQ 289
DB 238 RVEPCGCPCKRCRCPPELPGSPVFIFFPKPKDTLTISGPEVTCVVVDGQDDPEVQ 297
QY 290 FMYVYGVVHNAKTKEPBEQNFSTFRVYVLTVAHOMLNGKCYKCVNKGFLPAPIEK 349
DB 298 FSWFDVNEVTRAKTKPEBEQNSTFRVYVSLPIPHODMTGSKCKYVHNAALPAPIYR 357
QY 350 TISKTKGPREPOVYTLTPPSREEMTKNQVSLTCLVKGFPSPDIAVWESNGQP--ENNYK 407
DB 358 TISRKGGAREPOVYVLAPOBELSKSTLSVTLCTVGFYPOVIAVEMQNGQPBSEDKYG 417
QY 408 TTPPMLDSDGSFYLKSLTVDKSRMQGVNVSQSVMEALNNHYTKSLISLSPGK 462
DB 418 TTSQLDADGSYFLYSRLKVDKMSWQEGDTYACVVMHEALNNHYTKSLISLSPGK 472

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RESULT 12

PC4436
 monoclonal antibody 13-1 heavy chain - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
 C:Accession: PC4436
 R:Akashi, S.; Kato, K.; Toriawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.
 Biochem. Biophys. Res. Commun. 240, 566-572, 1997
 A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
 A:Reference number: JCS810; MUID:98063277; PMID:9398605
 A:Accession: PC4436
 A:Molecule type: protein
 A:Residues: 1-444 <AKA>
 A:Cross-references: UNIPARC:UPI0000176F41
 C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:251-320/Domain: immunoglobulin homology <IMM>
 F:22/Disulfide bonds: interchain (to 98) #status predicted
 F:199/Disulfide bonds: interchain (to 109) #status predicted

Query Match 57.4%; Score 1430.5; DB 2; Length 444;
 Best Local Similarity 59.4%; Pred. No. 1.4e-75;
 Matches 266; Conservative 75; Mismatches 98; Indels 9; Gaps 6;

```

QY 20 EVOLQSGPELVKPGASVMSCKASGYGTDTYYIHMMKQSHKSLIEWIGYI--YPPNGCN 77
DB 1 EVQAVETGGVLRPNQSLKSLTSGFSPNSYRHHMNLQPPGKRLIEWLAVITVSKDNGA 60
QY 78 GYNQFKGKATLTVDKSSSTAYMEKRLTSEDSAVYYCGRSTW--DDPYMGQTTLTVSS 136
DB 61 KYAESVRGRTISRDSKSSVYLQWNRLEEDATAYCCRTPWVAVMDCWQGGTSTVIYS 120
QY 137 ASTGSPVPLAPCSRSTSESTALGCLVKQYFPPVTVSNNSGALTSQVHTFPAVLQSS 196
DB 121 AKTPPSVYPLAPGSAQTNSMTVTLGCLVKGFPPEPVTVNMSGSLSGVHTFPAVLQSD 180
QY 197 GLYSLSVTVTPSSNFGTQTYTCNVDRKPSNTKVDKTVERKCCVCEPP--CPAPVAGPS 254
DB 181 -LYTSSSVTVTPSSRWSEPEYTCNVAPASSTKVDKTLVPRDC--GCKXCICVPEVS--S 236
QY 255 VFLPPEPKDITLMISRPETVCVVVDVSHDEPVQFNNYVDGVEVNAKTKPREQFNST 314
DB 227 VFIPPEPKDVLITTLTLPKVCVVVDISKDDPEVQFSWFDVDEVHTAQTPREQFNST 296
QY 315 FRVSVTLVAHQDMLNGEKYCKVSNKGLPAPIEKTISKTGQPREPOVYTLTPSREEMT 374
DB 297 FRVSSELPIMHQDMLNGEYFCRVNSAFAPIEKTISKTKGRPPAPQVYTIPLPEKQWA 356
QY 375 KNOVSLTCLVGFYPSDIAVWESNGQPENNYKTPPMLDSDGSFYLKSLTVDKSRMQQ 434
DB 357 KOKVSLTCLMTDFPEPDTTVEKQNGQPAEYKATQPIMDTDSIFVISKLVNQSNNMEA 416
QY 435 GNVSQSVMEALNNHYTKSLISLSPGK 462
DB 417 GNTFTCSVLHGLNNHHTKSLISLSPGK 444

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RESULT 13

IG heavy chain V region precursor - human
 S69339
 C:Species: Homo sapiens (man)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
 C:Accession: S69339; S72664
 R:Khamilich, A.A.; Autocourier, P.; Preud'homme, J.L.; Cogne, M.
 Eur. J. Biochem. 229, 54-60, 1995
 A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
 A:Reference number: S69339; MUID:95262687; PMID:7744049
 A:Accession: S69339
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-374 <KHA>
 A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695
 R:Khamilich, A.A.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S72664
 A:Accession: S72664
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-140, 'C', 142-374 <KH2>
 A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695
 C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 52.9%; Score 1316; DB 2; Length 374;
 Best Local Similarity 56.0%; Pred. No. 4.7e-69;
 Matches 263; Conservative 41; Mismatches 62; Indels 104; Gaps 7;

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QY 1 MECSWMLFLISGAGVISEVOLQSGELVPGASVMSCKASGY--TGTDYTIHMMKQ 58
DB 1 MDILCTLLTLTISWVLSITLKESGPTLVKPTQLTCTFSGFSLSKSGVGWGIRO 60
QY 59 SHGSLIEWIGYTPNNGNGNGNQFKGKATLTVDKSSSTAYMEKRLTSEDSAVYYCGRS 118
DB 61 PPGQALEWLAIFMDQ-DKRYSPSLRTRTLTKDTSKNQVVLTMNVDPADATAYTCGS 119
QY 119 TWD-----DFPYMGQTTLTVSSASTKGPVPLAPCSRSTSESTALGCLVKQYFPPV 173

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Db 120 VEGYGGYRFRHSGOCTLVTS-----EP- 144
Qy 174 TVSNNSGALTSGVHTFPVAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKVDKT 233
Db 145 -----KSCDKTH----- 151
Qy 234 VRRKCCVECPPCPPAP-VAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNW 292
Db 152 -----TCPCPAPRLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNW 204
Qy 293 YVDGVEVNAKTKPREBOFNSTFRVSVTVVHODMLNGEKYCKVSNKGLPAPIEKTIS 352
Db 205 YVDGVEVNAKTKPREBOFNSTFRVSVTVVHODMLNGEKYCKVSNKGLPAPIEKTIS 264
Qy 353 KTKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESDNGQPENNYKTTTPM 412
Db 265 KAKGQPREPOVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVWESDNGQPENNYKTTTPV 324
Qy 413 LQSDGSFFLYSKLTVDKSRMQQGNVFCGVMEHALHNHYTQKSLSLSPGK 462
Db 325 LQSDGSFFLYSKLTVDKSRMQQGNVFCGVMEHALHNHYTQKSLSLSPGK 374

RESULT 14

147159
Ig gamma 2a chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47159
R:Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47159
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-References: UNIPARC:UPI0000115524; EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PI
A:Gene: IGG2a
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 51.0%; Score 1271; DB 2; Length 328;
Best Local Similarity 70.4%; Pred. No. 1.6e-66;
Matches 231; Conservative 40; Mismatches 55; Indels 2; Gaps 1;
Qy 137 ASTKGSVPPLAPCSRSTSESTALGCLVKDYFPPPVTVSNNSGALTSGVHTFPVAVLQSS 196
Db 1 AKTAPLVYPLAPCGSDTSGPNVALGCLASSYFPPEPVTVSNNSGALTSGVHTFPVAVLQSS 60
Qy 197 GLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVRRKCCVCPCCPAPVAGPSVF 256
Db 61 GLYSLSMTVTPASSLSKSYTCNVNHPATTTKVDKRGVGTKPKPCPCPACESPGPSVF 120
Qy 257 LPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 316
Db 121 IFFPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 180
Qy 317 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREEMTKN 376
Db 181 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREEMTKN 240
Qy 377 QVSLTCLVKGFYPSDIAVWESDNGQ--PENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQ 434
Db 241 KVSITCLVIGFPPIDVEMQNRNGQPREPGNRTITPPQDDVGGTFLYSKFSVDKASWQG 300
Qy 435 GNVFSCSVMEHALHNHYTQKSLSLSPGK 462
Db 301 GGIFQCAVMEHALHNHYTQKSLSLSPGK 328

RESULT 15

147160
Ig gamma 2b chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C:Accession: I47160
R:Kaczkovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a B
A:Reference number: I47158; MUID:95015845; PMID:7930579
A:Accession: I47160
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-328 <KAC>
A:Cross-References: UNIPARC:UPI0000115525; EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PI
A:Gene: IGG2b
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 50.8%; Score 1265; DB 2; Length 328;
Best Local Similarity 70.1%; Pred. No. 3.6e-66;
Matches 230; Conservative 39; Mismatches 57; Indels 2; Gaps 1;
Qy 137 ASTKGSVPPLAPCSRSTSESTALGCLVKDYFPPPVTVSNNSGALTSGVHTFPVAVLQSS 196
Db 1 AKTAPLVYPLAPCGSDTSGPNVALGCLASSYFPPEPVTVSNNSGALTSGVHTFPVAVLQSS 60
Qy 197 GLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVDKTVRRKCCVCPCCPAPVAGPSVF 256
Db 61 GLYSLSMTVTPASSLSKSYTCNVNHPATTTKVDKRGVGTKPKPCPCPACESPGPSVF 120
Qy 257 LPPPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 316
Db 121 IFFPKKDTLMSRTPEVTCVVVDVSHEDPEVQFNMYVDGVEVNAKTKPREBOFNSTFR 180
Qy 317 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREEMTKN 376
Db 181 VVSUVTLVHODMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREEMTKN 240
Qy 377 QVSLTCLVKGFYPSDIAVWESDNGQ--PENNYKTTTPMLDSGSFFLYSKLTVDKSRMQQ 434
Db 241 KVSITCLVIGFPPIDVEMQNRNGQPREPGNRTITPPQDDVGGTFLYSKFSVDKASWQG 300
Qy 435 GNVFSCSVMEHALHNHYTQKSLSLSPGK 462
Db 301 GGIFQCAVMEHALHNHYTQKSLSLSPGK 328

Search completed: January 24, 2006, 18:57:19
Job time : 33.3863 secs


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Db      180 NSGALTSVHTPPAVLQSSGLYSLSVTVVTVSSNFGTQTYTCNVHKKPNTKVTVERK 239
Qy      238 CCVECPCCPAPVAGSVLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVQFNMYVDQ 297
Db      240 CCVECPCCPAPVAGSVLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVQFNMYVDQ 299
Qy      298 EVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIETKTISKTKQ 357
Db      300 EVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIETKTISKTKQ 359
Qy      358 PREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPMLDSDG 417
Db      360 PREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPMLDSDG 419
Qy      418 SFFLYSKLTVDKSRMOQGNVFCSCVHMEALHNNHTQKSLSLSPGK 462
Db      420 SFFLYSKLTVDKSRMOQGNVFCSCVHMEALHNNHTQKSLSLSPGK 464

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RESULT 2

068CN4 HUMAN PRELIMINARY; PRT; 470 AA.

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ID      068CN4
AC      068CN4
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE      Hypothetical protein DKFp666E23209.
GN      Name=DKFp666E23209;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Rectum tumor;
RG      The German cDNA Consortium;
RA      Bloecher H., Boecher M., Brandt P., Neues H.W., Weill B., Amid C.,
RA      Osaenger A., Fobo G., Han M., Wiemann S.;
RA      Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR      EMBL; CR749861; CAH18705.2; -; mRNA.
DR      SMR; 068CN4; 43-493.
GO      GO:0016021; C:Integral to membrane; IEA.
DR      InterPro; IPR003559; I9.
DR      InterPro; IPR007110; I9-1like.
DR      InterPro; IPR003597; I9_C1.
DR      InterPro; IPR003006; I9_MHC.
DR      InterPro; IPR003596; I9_Y.
DR      Pfam; PF07654; C1-sec; 3.
DR      SMART; SM00409; I9; 2.
DR      SMART; SM00407; I9C1; 3.
DR      SMART; SM00406; I9C1; 1.
DR      PROSITE; PSS0835; IG_LIKE; 4.
DR      PROSITE; PSS0290; IG_MHC; UNKNOWN 2.
KW      Hypothetical protein.
SQ      SEQUENCE 470 AA; 51536 MW; 7CB061DFC03D0B2B CRC64;

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Query Match 81.7%; Score 2035; DB 2; Length 470;

Best Local Similarity 81.5%; Pred. No. 1.8e-133;

Matches 383; Conservative 27; Mismatches 52; Indels 8; Gaps 2;

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Qy      1 MECSCVMLFLBSGTAGVLSRVDLQSGPELVKGSVKNKSCRAAGYTGDTYYIHNMKQSH 60
Db      1 MEFGLSWVFLVALLRVCQVQVQVDSGGGVQPGKSVRLSCAASGDFSTYAMHWVRQSP 60
Qy      61 GKSLEWIGYIYPPNNGANGYNQKFKGATLTVDKSSSTAYMEI.LTLTSDSANYTCGR--- 117
Db      61 GRLLEWVAIVSYRGKQHTADSVKGAATISRDNSMKTVALQLSGLSTEDTGYVYCAKADPL 120
Qy      118 --STWDP---FDYMGQGTLLTVVSSASTKGPVFPPLAPCSRSTSESTAAAGCIVKQYFPP 172
Db      121 PLSSHTNTYALDVWGQGTAVIVSSASTKGPVFPPLAPCSRSTSESTAAAGCIVKQYFPP 180

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Qy      173 VTVSNNSGALTSGVHTPPAVLQSSGLYSLSVTVVTVSSNFGTQTYTCNVHKKPNTKVDK 232
Db      181 VTVSNNSGALTSGVHTPPAVLQSSGLYSLSVTVVTVSSNFGTQTYTCNVHKKPNTKVDK 240
Qy      233 TVBERCCVCECPCCPAPVAGSVLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVQFN 292
Db      241 TVBERCCVCECPCCPAPVAGSVLFPKPKDPTLMISRTPEVTCVVVDVSHEDDEVQFN 300
Qy      293 YVDGVEVNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIETKTIS 352
Db      301 YVDGVEVNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYCKVSNKGLPAPIETKTIS 360
Qy      353 KTKGQPREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPM 412
Db      361 KTKGQPREPQVYTLPPSREEMTKQVSLTCLVKGFPSPDIAVEMESNGQPENNYKTPPM 420
Qy      413 LDSGSPFLYSLKLTVDKSRMOQGNVFCSCVHMEALHNNHTQKSLSLSPGK 462
Db      421 LDSGSPFLYSLKLTVDKSRMOQGNVFCSCVHMEALHNNHTQKSLSLSPGK 470

```

RESULT 3

068C4 HUMAN PRELIMINARY; PRT; 465 AA.

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ID      068C4
AC      068C4
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Hypothetical protein.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC      Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RG      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raza S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Roark S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalhus D.B.,
RA      Scherch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences."
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN      [2]
RP      NUCLEOTIDE SEQUENCE.
RC      TISSUE=Spleen;
RG      Straussberg R.;
RA      Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR      EMBL; BC062335; AA62335.1; -; mRNA.
DR      HSP; P01861; IADQ.
DR      SMR; 068C4; 20-465.
DR      InterPro; IPR003599; I9.
DR      InterPro; IPR007110; I9-1like.
DR      InterPro; IPR003597; I9_C1.
DR      InterPro; IPR003006; I9_MHC.
DR      InterPro; IPR003596; I9_Y.
DR      Pfam; PF07654; C1-sec; 3.

```


DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37E6D CRC64;

Query Match 81.3%; Score 2025.5; DB 2; Length 465;
 Best Local Similarity 81.3%; Pred. No. 8.2e-133;
 Matches 378; Conservative 32; Mismatches 52; Indels 3; Gaps 1;

QY 1 MECSWMLFLSAGTAVLSEVQLQSGPELVKPGASVMSCKASGYTDTYIHMMKQSH 60
 DB 1 MELGNWLVLAILEGVCCEVQLMSAGLVKPGSLSLSCASAFPPESEVMASVVRQAP 60
 QY 61 GKSLWIGYIYPPNNGNGYNOKFKKATLTVDKSSSTAYMELRTLTSDSAVYTCGRSTW 120
 DB 61 GKLEWVANIKDGSATYHLSVKGRFTISRDNANNTYTLQWNSLRVEDTAYYCARETP 120
 QY 121 DD---FDWGGGTTLVSSASTKGPSVFPPLACSRSTSESTALGCLVKDYFPEPVTSW 177
 DB 121 GGRCTYDWMHGCTLVSSASTKGPSVFPPLACSRSTSESTALGCLVKDYFPEPVTSW 180
 QY 178 NSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKTVBRK 237
 DB 181 NSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKTVBRK 240
 QY 238 CCVECPCPAPPAVPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFNNYVDGV 297
 DB 241 CCVECPCPAPPAVPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFNNYVDGV 300
 QY 298 EVHNAKTPREBOFNSTFRVSVLTVMHODMLNGEKYCKVSNKGLPAPIETKTSKTQ 357
 DB 301 EVHNAKTPREBOFNSTFRVSVLTVMHODMLNGEKYCKVSNKGLPAPIETKTSKTQ 360
 QY 358 PREPVYTLTPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNGCPENNYKTPPMLDSG 417
 DB 361 PREPVYTLTPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNGCPENNYKTPPMLDSG 420
 QY 418 SFFLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSISPGK 462
 DB 421 SFFLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSISPGK 465

RESULT 4
 Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.

ID Q7Z7P5 HUMAN PRELIMINARY; PRT; 469 AA.
 AC Q7Z7P5;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=SpLeen.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares W.B., Bonaldo M.F., Casavant T.L., Schetz T.R.,
 RA Brownstein M.J., Ueda T.B., Toshitaki S., Carninci P., Prange C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=SpLeen.
 RG NIH MGC Project;
 RL Submitted (Apr-2003) to the EMBL/Genbank/DBJ databases.
 DR EMBL; BC051328; AAH51328.1; mRNA.
 DR HSSP; P01857; 1H2H.
 DR SMR; Q7Z7P5; 20-469.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Immunoglobulin domain.
 SQ SEQUENCE 469 AA; 51395 MW; C6D5BE12BAAP795C CRC64;

Query Match 78.8%; Score 1962.5; DB 2; Length 469;
 Best Local Similarity 78.5%; Pred. No. 2.1e-128;
 Matches 368; Conservative 42; Mismatches 52; Indels 7; Gaps 3;

QY 1 MECSWMLFLSAGTAVLSEVQLQSGPELVKPGASVMSCKASGYTDTYIHMMKQSH 60
 DB 1 MDWTSLIFLVAATGAPVQHLVQSGAEVKKPGASVLSCKTSQGNSSYDLIWRQAP 60
 QY 61 GKSLWIGYIYPPNNGNGYNOKFKKATLTVDKSSSTAYMELRTLTSDSAVYTCGRSTW 117
 DB 61 GKLEWVANIKDGSATYHLSVKGRFTISRDNANNTYTLQWNSLRVEDTAYYCARETP 120
 QY 118 STWDFDYWGCGTTLVSSASTKGPSVFPPLACSRSTSESTALGCLVKDYFPEPVTSW 177
 DB 121 GQVDFDWMGGCTLVSSASTKGPSVFPPLACSRSTSESTALGCLVKDYFPEPVTSW 180
 QY 178 NSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKTVBRK 237
 DB 181 NSGALTSGVHTFPFPAVLQSSGLYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKTVBRK 240
 QY 238 CCVE---CPCPAPPAVPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFNNYVDGV 293
 DB 241 SCDKTHCTPCPAPPAVPSVFLFPKPKDITLMSRTPEVTCVVVDVSHEDPEVFNNYVDGV 300
 QY 294 VDGVEVHNAKTPREBOFNSTFRVSVLTVMHODMLNGEKYCKVSNKGLPAPIETKTSK 353
 DB 301 VDGVEVHNAKTPREBOFNSTFRVSVLTVMHODMLNGEKYCKVSNKGLPAPIETKTSK 360
 QY 354 TKGQPREPVYTLTPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNGCPENNYKTPPML 413
 DB 361 AKGQPREPVYTLTPSREEMTKNOVSLTCLVKGFYPSDIAVEMESNGCPENNYKTPPML 420
 QY 414 DSDGSFPLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSISPGK 462
 DB 421 DSDGSFPLYSKLTVDKSRWQGNVPSGSVMHEALHNHYTQKSLSISPGK 469

RESULT 5

ID Q6N030 HUMAN PRELIMINARY; PRT; 518 AA.
 AC Q6N030;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686i15212.

GN Name=DKFZp686i15212;

OS Homo sapiens (Human).

OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC NCBI_TaxID=9606;

OK NCBI_TaxID=9606;

RN NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RC Tissue=Rectum tumor;

RG The German cDNA Consortium;

RA Poulack A., Albert R., Moosmayer P., Schnupp I., Wellenreuther R.,

RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640724; CAE45841.1; -; mRNA.

DR HSSP; P01861; IADQ.

DR InterPro; IPR000005; HTHARAC.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.

DR PROSITE; PS00835; IG LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

DR Hypothetical protein.

KW Hypothetical protein.

SO SEQUENCE 518 AA; 57019 MW; 93B5F96813BF6382 CRC64;

Query Match 78.6%; Score 1958; DB 2; Length 518;

Best Local Similarity 73.0%; Pred. No. 4.8e-128;

Matches 378; Conservative 37; Mismatches 47; Indels 56; Gaps 5;

QY 1 MECSVMFLSLSTAGVLSVVOLOQSGPFLVPGASVYKMSCTASGTTGDTYIIMMKOSH 60
DB 1 MDMTRILFLVLAATGAHSGVHLYVSGAEVKKPGASVKSCTASGTPFNHINWVRCAP 60
QY 61 GKSLEWIGIYIPNNGNGYNOKEFKGKATLTVDKSSATAMELRTLSDESAVYCGRS-- 118
DB 61 GQSLHEWIGINTGNGTKTSQKFGQVITTRDTMTTAAWDLSSLSSTAVYWCARDAP 120
QY 119 ---TWDDPDYWGQITLTVSSASTKGPVPLAPCSRSTSESTALGLVNDYFPEPVY 175
DB 121 GQVTTTTPDYWGQITLTVSSASTKGPVPLAPCSRSTSESTALGLVNDYFPEPVY 180
QY 176 SNNSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSNTKVDKYE 235
DB 181 SNNSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSNTKVDKYE 240
QY 236 RK-----C-CYE-----CPC 245
DB 241 LKTPGLADTHTTCPC 300
QY 246 PAPP-VAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPQVFNWYVDGVEVNAKT 304
DB 301 PAPPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHDEPQVFNWYVDGVEVNAKT 360
QY 305 KRRBEPNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPIEKTISTKQPREPVY 364
DB 361 KRRBEPNSTFRVYVLTIVHODMLNGSKYCKVSNKGLPAPIEKTISTKQPREPVY 420
QY 365 TLPRSEEMTKNOVSLTCLVKGFPYSDIAVEMSNQPENNYKTPPMILDSGSPFLYK 424
DB 421 TLPRSEEMTKNOVSLTCLVKGFPYSDIAVEMSNQPENNYKTPPMILDSGSPFLYK 480
QY 425 LTVDKSRMOQGNVFCVSHALHNYTOKSLISLSPGK 462
DB 481 LTVDKSRMOQGNVFCVSHALHNYTOKSLISLSPGK 518

RESULT 6

Q6N093_HUMAN

AC Q6N093;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein DKFZp686i04196 (fragment).

GN Name=DKFZp686i04196;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

OK NCBI_TaxID=9606;

RN NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.

RC Tissue=Human esophagus tumor;

RG The German Human cDNA Consortium;

RA Wamut R., Heubner D., Meves H.W., Weil B., Amd C., Osanger A.,

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BX640623; CAR45777.1; -; mRNA.

DR HSSP; P01861; IADQ.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig-cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig V.

DR Pfam; PF07654; Cl-set; 3.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG LIKE; 3.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

DR Hypothetical protein.

KW Hypothetical protein.

FT NON TER 1

SO SEQUENCE 417 AA; 46061 MW; C4518B844CFB883C CRC64;

Query Match 78.5%; Score 1955; DB 2; Length 417;

Best Local Similarity 87.5%; Pred. No. 5.9e-128;

Matches 363; Conservative 20; Mismatches 30; Indels 2; Gaps 1;

QY 50 DYIIMMFGSHGKSLSEWIGIYIPNNGNGYNOKEFKGKATLTVDKSSATAMELRTLSDE 109
DB 3 NYAMHMTVQAPKPKGLEWYAVLAYDSQYVADSVGRFTVSRDNTLFLFEMSLRDE 62
QY 110 SAVVYCGR--STWDDPDYWGQITLTVSSASTKGPVPLAPCSRSTSESTALGLVND 167
DB 63 TAVVYCAHAGSTSFDPWGQITLTVSSASTKGPVPLAPCSRSTSESTALGLVND 122
QY 168 YFPEPVTVSNNSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSN 227
DB 123 YFPEPVTVSNNSGALTSQVHTFPVAVLOSGLYSLSSVYTPSSNFGTQYTCNVNDKPSN 182
QY 228 TKVDKTVBRKCCVCEPCPCAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHDEP 287
DB 183 TKVDKTVBRKCCVCEPCPCAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHDEP 242
QY 288 VQFNMYVGVGVHNAKTPREQFNSFRVYVLTIVHODMLNGSKYCKVSNKGLPAPI 347
DB 243 VQFNMYVGVGVHNAKTPREQFNSFRVYVLTIVHODMLNGSKYCKVSNKGLPAPI 302
QY 348 EKTISTKQPREPVYTLPRSEEMTKNOVSLTCLVKGFPYSDIAVEMSNQPENNYK 407
DB 303 EKTISTKQPREPVYTLPRSEEMTKNOVSLTCLVKGFPYSDIAVEMSNQPENNYK 362
QY 408 TTPPMLDSDGSPFLYKLTVDKSRMOQGNVFCVSHALHNYTOKSLISLSPGK 462
DB 363 TTPPMLDSDGSPFLYKLTVDKSRMOQGNVFCVSHALHNYTOKSLISLSPGK 417

RESULT 7

Q6N093_HUMAN

ID Q6N095 HUMAN PRELIMINARY; PRT; 475 AA.
 AC Q6N095;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686K03196.
 GN Name=DKFZp686K03196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Esophagus tumor;
 RG The German cDNA Consortium;
 RA Wandtke R., Heubner D., Mewes H.W., Weil B., Amlid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640621; CA645775.1; -, mRNA.
 DR HSSP; P01861; IADO.
 DR SMR; Q6N095; 20-475.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003597; IG-1-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 475 AA; 52360 MW; 7BA14104CD2DB8F0 CRC64;

 Query Match 78.3%; Score 1950.5; DB 2; Length 475;
 Best Local Similarity 79.2%; Pred. No. 1,4e-127;
 Matches 369; Conservative 37; Mismatches 47; Indels 13; Gaps 4;

RESULT 8
 ID Q5EBM2 HUMAN PRELIMINARY; PRT; 519 AA.
 AC Q5EBM2;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN Name=DKFZp686K03196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RG MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Lymph;
 RG Director MGC Project;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC089421; AA089421.1; -, mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-1-like.
 DR InterPro; IPR003597; IG-1-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; CI-set; 3.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KM Hypothetical protein.
 SQ SEQUENCE 519 AA; 56813 MW; 988C5C2P92B9E34C CRC64;

 Query Match 78.0%; Score 1942.5; DB 2; Length 519;
 Best Local Similarity 72.3%; Pred. No. 5.8e-127;
 Matches 375; Conservative 34; Mismatches 53; Indels 57; Gaps 5;

QY 175 VSMNGALTSVHTPPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVCHKPENTIVDKTV 234
 DB 181 VSMNGALTSVHTPPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVCHKPENTIVDKTV 240
 QY 235 ERK-----C-CVE-----C-CP 244
 DB 241 ELKTLPGDTTTCPCRCPEPKSCDTPPCRCPEPKSCDTPPCRCPEPKSCDTPPCPR 300
 QY 245 CPAPP-VAGPSVFLPPPKKDTLMISRTPEVTGVVVDVSHEDPEVGFNNYVGVGVHNAK 303
 DB 301 CPAPELGSPSVFLPPPKKDTLMISRTPEVTGVVVDVSHEDPEVGFNNYVGVGVHNAK 360
 QY 304 TKPREBQNSTFRVSVLTIVHODWLNKGYCKVSNKGLPAPIEKTISKTKGQPREPOV 363
 DB 361 TKPREBQNSTFRVSVLTIVHODWLNKGYCKVSNKGLPAPIEKTISKTKGQPREPOV 420
 QY 364 YTLPPSREEMTKNOVSLTCLVNGFYPSPDIIVEMESGQPENNYKTPMLDSDGSEFLYS 423
 DB 421 YTLPPSREEMTKNOVSLTCLVNGFYPSPDIIVEMESGQPENNYKTPMLDSDGSEFLYS 480
 QY 424 KLTVDKSRMOQGNVFCSCVMHEALHNHYTKOKSLSPGK 462
 DB 481 KLTVDKSRMOQGNVFCSCVMHEALHNHYTKOKSLSPGK 519

RESULT 9

06PUF1 HUMAN PRELIMINARY; PRT; 480 AA.

AC 06PUF1; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Mullany S.J.,
 RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodighiero S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scheraga A., Schein J.E., Jones S.J.M., Maitra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lung;
 RA Strausberg R.L.;
 RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC016381; AAH16381.1; -, mRNA.
 DR HSSP; P01861; IADO.
 DR InterPro; IPR003559; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGc1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 480 AA; 52586 MW; 64DC641AE47CD6C8 CRC64;

Query Match 77.9%; Score 1940; DB 2; Length 480;
 Best Local Similarity 77.3%; Pred. No. 7.8e-127;
 Matches 371; Conservative 35; Mismatches 56; Indels 18; Gaps 4;

QY 1 MECSVMFLSGTGVLSVQLQSGPELVFGASVMSKASGTYGDIYHMKQSH 60
 DB 1 MDWTRFLFVVAALAGVQSVQLVQSGAEVKKRGSVAVSCASGSGPSFIVSVRQAP 60
 QY 61 GKSLKEMIGYIPNNGNGNGNOKFKKATLVQKSSSTAYMELRTLTSDSAVYTCR--- 117
 DB 61 GGGGLAMWGIIIPAFDITKVAQNFQDRVITSADESTDTAMELRSLRSEDTATYCARDIA 120
 QY 118 ---STWDDF-----DYWGQGITLVYSASTKPSVFPPLACRSSTSESTALGCLVK 166
 DB 121 EYELMSGFTDEKXYGLVWVGQGTPTVSSASTKPSVFPPLACRSSTSESTALGCLVK 180
 QY 167 DYFPPPTVSMNSGALTSVHTPPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVCHKPS 226
 DB 181 DYFPPPTVSMNSGALTSVHTPPAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVCHKPS 240
 QY 227 NTKVDKTKERKCCVE---CPPCAPP-VAGPSVFLPPPKKDTLMISRTPEVTGVVVDV 282
 DB 241 NTKVDKTKERKCCVE---CPPCAPP-VAGPSVFLPPPKKDTLMISRTPEVTGVVVDV 300
 QY 283 HEDPEVQRMVYDGVYHNAAKTKPREBQNSTFRVSVLTIVHODWLNKGYCKVSNKGL 342
 DB 301 HEDPEVQRMVYDGVYHNAAKTKPREBQNSTFRVSVLTIVHODWLNKGYCKVSNKGL 360
 QY 343 LPAPIEKTISKTKGQPREPOVTLTPPSREEMTKNOVSLTCLVNGFYPSPDIIVEMESGQ 402
 DB 361 LPAPIEKTISKTKGQPREPOVTLTPPSREEMTKNOVSLTCLVNGFYPSPDIIVEMESGQ 420
 QY 403 ENNYKTPMLDSDGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKOKSLSPGK 462
 DB 421 ENNYKTPMLDSDGSEFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKOKSLSPGK 480

RESULT 10

06GMX6 HUMAN PRELIMINARY; PRT; 465 AA.

AC 06GMX6; 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RA MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abrahams R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -, mRNA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKOWN_2.
DR Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 77.3%; Score 1924.5; DB 2; Length 465;
Best Local Similarity 78.9%; Pred. No. 9e-126;
Matches 362; Conservative 37; Mismatches 55; Indels 5; Gaps 3;

QY 8 LFLISGTAGVLSSEVLOQSGPELVKPGASVWMSCKASGYGTDYIHHMKOSHGLKLEMI 67
DB 8 LILVAPAPRWVLSQVLOQSGPELVKPGASVWMSCKASGYGTDYIHHMKOSHGLKLEMI 67
QY 68 GYIYVNNNGNGYNGQFKGKATLVVKSSTAYMEIRTLTSEDSAVYVYCGRTWDDPDYWG 127
DB 68 GRIT-TSGSTNNPBLKSRVMSVDTSKNQPSLKSSVTAADTAYVYCARGRFTYFDYWG 126
QY 128 OGTTLVVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPPEVTVVSWNSGALTSGVH 187
DB 127 OGTLVTVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPPEVTVVSWNSGALTSGVH 186
QY 188 TEPVALQSSGLYSLSVTVVPPSSNFGTQYTCNVNHHKPSNTKVDKTVKCCV---CPR 244
DB 187 TEPVALQSSGLYSLSVTVVPPSSNFGTQYTCNVNHHKPSNTKVDKTVKCCV---CPR 246
QY 245 CPAPV-VAGPSVFLPPPKKDTLMTSRTPVYTCVVDVSHEDPEVQFNMYVDGVEVHNAK 303
DB 247 CPAPELGSPSFLPPPKKDTLMTSRTPVYTCVVDVSHEDPEVQFNMYVDGVEVHNAK 306
QY 304 TKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKTKGPREPQV 363
DB 307 TKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISKTKGPREPQV 366
QY 364 YTLPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQENNYKTPPMLDSDSPFLYS 423
DB 367 YTLPSRDLTKNOVSLTCLVKGFPYPSDIAVEMNSGQENNYKTPPVLDSGSPFLYS 426
QY 424 KLTVDKSRWQGNVSCSVMEHALNHYTKSLSPGK 462
DB 427 KLTVDKSRWQGNVSCSVMEHALNHYTKSLSPGK 465

RESULT 11
Q569F4 HUMAN
ID Q569F4_HUMAN PRELIMINARY; PRT; 469 AA.

AC Q569F4;
DT 10-MAY-2005 (Tremblrel. 30, Created)
DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carroll P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Lymph;
RG NIH MGC Project;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC092518; AAH92518.1; -, mRNA.
SQ SEQUENCE 469 AA; 51254 MW; AC13448E3047784F CRC64;

Query Match 77.2%; Score 1922.5; DB 2; Length 469;
Best Local Similarity 77.4%; Pred. No. 1.3e-125;
Matches 364; Conservative 41; Mismatches 56; Indels 9; Gaps 4;

QY 1 MECSVLMFLISGTAGVLSSEVLOQSGPELVKPGASVWMSCKASGYGTDYIHHMKOSH 60
DB 1 MEFGLSWFLVAILKGVQCEVQVYSSGCVVQPGSLSLSCAAGFTTDDVMHVRQAP 60
QY 61 GKSLIEWIGYIYVNNNGNGYNGQFKGKATLVVKSSTAYMEIRTLTSEDSAVYVYCG 116
DB 61 GKSLIEWVLSISWDGSTYVADSVKGRFTISDRNSKNSLYLQNNSLRABDTALYYCATRGS 120
QY 117 RSTWDDPEVWGGTTLTVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPPEVTVV 176
DB 121 YST-AGFYVGGTTLTVSSASTKGSVPFLAPCSRSTSESTALGCLVQDYPPEVTVV 179
QY 177 WNSGALTSGVHTFPVALQSSGLYSLSVTVVPPSSNFGTQYTCNVNHHKPSNTKVDKTV 236
DB 180 WNSGALTSGVHTFPVALQSSGLYSLSVTVVPPSSNFGTQYTCNVNHHKPSNTKVDKTV 239
QY 237 KCVE---CPCPAPV-VAGPSVFLPPPKKDTLMTSRTPVYTCVVDVSHEDPEVQFN 292
DB 240 KSCDTHKCPCPAPELGSPSFLPPPKKDTLMTSRTPVYTCVVDVSHEDPEVQFN 299
QY 293 YVDGVEVHNATKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISK 352
DB 300 YVDGVEVHNATKPREQENSTFRVSVLTIVHODWLNGKVKCVSNKGLPAPIEKTISK 359
QY 353 KTKGPREPQVYTLPSREEMTKNOVSLTCLVKGFPYPSDIAVEMNSGQENNYKTPPML 412

Db 360 KAKGQPREQVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMSGNPENNYKTTTPV 419
Qy 413 LDDSDGFLLYSKLTVDKSRMOQGNVFCSCVMHEALNNHYTKSLSPK 462
Db 420 LDDSDGFLLYSKLTVDKSRMOQGNVFCSCVMHEALNNHYTKSLSPK 469

RESULT 12

Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
ID Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
GN Name=DKFZp686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Wambolt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -; mRNA.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein
KW SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;
SQ

Query Match 77.2%; Score 1922; DB 2; Length 472;
Best Local Similarity 76.7%; Pred. No. 1.4e-125;
Matches 362; Conservative 41; Mismatches 59; Indels 10; Gaps 3;

Qy 1 MEGSCVMFLISGTAGVLSVLOQSGPELVKPGASVKNMCKASGYTGTDYTIHMKQSH 60
Db 1 MEIGLTMIFLAILKGVOCHEVOLVESGGGLVOPGRLRLSCAASGFTPDYAMHWVRQAP 60
Qy 61 GKSLEWIGYIPNNGNGYNOKFKGKATLTVDKSSSTAYMEIRLTSEDSAYVYCGRS- 119
Db 61 GKGLEWVSGISNMSSGIAVADSVKGFITSRDGNKSLYLQMSLAEADTALTYCKAEIG 120
Qy 120 -----WDPEYMGQGTTLTVSSASTKGPSVFPLAAPSSTSTALAGCLVNDYFPEPYT 174
Db 121 AHHFYGYMDVWGQGTTLTVSSASTKGPSVFPLAAPSSTSTALAGCLVNDYFPEPYT 180
Qy 175 VSMNSGALISGHTTFAVLOSGSLYSLSVYVYPSNFGTQYTCNVDHKPSNTKDKTV 234
Db 181 VMNSGALISGHTTFAVLOSGSLYSLSVYVYPSNFGTQYTCNVNHKPSNTKDKTV 240
Qy 235 ERKCYE---CPKCPAP--VAGPSVFLPPKPKDITMISRTPEVTCVVVDVSHEDPEVQ 290
Db 241 EPKSCDKITTPCPKCPAPBELGSPVFLPPKPKDITMISRTPEVTCVVVDVSHEDPEVQ 300
Qy 291 NMYVDGVEVNAKTKRREQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETK 350
Db 301 NMYVDGVEVNAKTKRREQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETK 360
Qy 351 ISKTKQPREPOVYTLTPPSREEMTKNOVSLTCLVKGFPSPDIAVEMSGNPENNYKTTTP 410

Db 361 ISKAKGQPREPOVYTLTPPSRDELTKNOVSLTCLVKGFPSPDIAVEMSGNPENNYKTTTP 420
Qy 411 PMLDDSGFFLLYSKLTVDKSRMOQGNVFCSCVMHEALNNHYTKSLSPK 462
Db 421 PMLDDSGFFLLYSKLTVDKSRMOQGNVFCSCVMHEALNNHYTKSLSPK 472

RESULT 13

Q5RE17 PONPY PRELIMINARY; PRT; 475 AA.
ID Q5RE17 PONPY PRELIMINARY; PRT; 475 AA.
AC Q5RE17;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Hypothetical protein DKFZp469C2335.
GN Name=DKFZp469C2335;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RG The German cDNA Consortium;
RA Poulet A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR857722; CAH89990.1; -; mRNA.
DR SRR; Q5RE17; 21-475.
DR GO; GO:0010106; F:MHC class I receptor activity; IEA.
DR GO; GO:0019883; P:antigen presentation, endogenous antigen; IEA.
DR GO; GO:0019885; P:antigen processing, endogenous antigen via . . .; IEA.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_C1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IG1; 3.
DR SMART; SM00406; IG1; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS50290; IG_MHC; UNKNOWN_2.
DR Hypothetical protein
KW SEQUENCE 475 AA; 51898 MW; 04BBD096A2CD529 CRC64;
SQ

Query Match 76.7%; Score 1910.5; DB 2; Length 475;
Best Local Similarity 77.0%; Pred. No. 8.8e-125;
Matches 361; Conservative 35; Mismatches 60; Indels 13; Gaps 3;

Qy 7 MFLISGTAGVLSVLOQSGPELVKPGASVKNMCKASGYTGTDYTIHMKQSHQKSLM 66
Db 7 IALLAVTQACADQLQVDSGLAEVKGPGESLRLCKGSGYTTTDWIGKVRQPKGLEL 66
Qy 67 IGYIPNNGNGYNOKFKGKATLTVDKSSSTAYMEIRLTSEDSAYVYCGRS- 122
Db 67 MCMIDPSNSGTYKNSFSFGLITISADWISITAVLQMTSLKADSAIYCARLRISGTNSY 126
Qy 123 -----FDYMGQGTTLTVSSASTKGPSVFPLAAPSSTSTSTALAGCLVNDYFPEPYT 177
Db 127 HRSYFQFGQGTTLTVSSASTKGPSVFPLAAPSSTSTSTALAGCLVNDYFPEPYT 186
Qy 178 NSGALISGHTTFAVLOSGSLYSLSVYVYPSNFGTQYTCNVDHKPSNTKDKTV 237
Db 187 NSGALISGHTTFAVLOSGSLYSLSVYVYPSNFGTQYTCNVDHKPSNTKDKTV 246
Qy 238 CC---VECPKCPAP--VAGPSVFLPPKPKDITMISRTPEVTCVVVDVSHEDPEVQFNNY 293
Db 247 SCDTRPSCPAPBELGSPVFLPPKPKDITMISRTPEVTCVVVDVSHEDPEVQFNNY 306
Qy 294 VDGVEVNAKTKRREQFNSTFRVSVLTIVHODMLNGEKYCKVSNKGLPAPIETK 353

Db 307 VDVGEVHNAKTKPREBQNSSTFRVSVYLAHVQDMLNGKXKCVSNKALPAPIEKTISK 366
 Qy 354 TKGGPREPOVYTLPPSRBEMTKNOVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPM 413
 Db 367 AKGGPREPOVYTLPPSRBELTKNOVSLCLVKGFPSPDIAVWESSGGPPENNYKTTTPVL 426
 Qy 414 DSDGSFFLYSKLTVDKSRMOQGNVSCSVHMEALHNHYTKSLSPGK 462
 Db 427 DSDGSFFLYSKLTVDKSRMOQGNVSCSVHMEALHNHYTKSLSPGK 475
 RESULT 14
 O6PJ44 HUMAN PRELIMINARY; PRT; 470 AA.
 ID O6PJ44 HUMAN PRELIMINARY; PRT; 470 AA.
 AC O6PJ44
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE IGHG1 protein.
 GN Name=IGHG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Scherch A., Schein J.E., Jones S.J.M., Skalska U., Smalhus D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Primary B-Cells;
 RG NIH MGC Project;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL, BC018747; AAH18747.1; -, mRNA.
 DR HSP, F01861; LADQ.
 DR SMR, Q6PJ44; 20-470.
 DR InterPro: IPR003599; IG.
 DR InterPro: IPR007110; IG-like.
 DR InterPro: IPR003597; IG-cl.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003596; IG_v.
 DR Pfam: PF07654; Cl-sec; 3.
 DR SMART, SM00409; IG; 2.
 DR SMART, SM00407; IGcl; 3.
 DR SMART, SM00406; IGV; 1.
 DR PROSITE, PS50835; IG LIKE; 4.
 DR PROSITE, PS00290; IG_MHC; UNKNOWN; 2.
 DR PROSITE, PS00290; IG_MHC; UNKNOWN; 2.
 SQ SEQUENCE 470 AA; 51716 MW; 7849556A11FD7D99 CRC64;

Matches 361; Conservative 43; Mismatches 58; Indels 8; Gaps 4;
 Qy 1 MECSVMFLISGTAAGVSEVLOOQSGPEIKRPGASVMSKASGYTGDDYIHHMKOSH 60
 Db 1 MELGISWFLVAILLEGVCEVQLVSGGLVQPGSLSCVSGFTTSYSSMNSVRQAP 60
 Qy 61 GKSLEIGIYIPNNNGNGYNKFKGKATLTVDKSSSTYMEIRLTLSBDAVYCGR--S 118
 Db 61 GKGLEVMANIKQDGEKTKYVSVKGRFTISDNANSLYLQWNSLRADLTAYVCARDOS 120
 Qy 119 TW--DDPDYWGQITLTVSSASTKGPVPLAPCSRSTSESTALGCLVKYDPPRPVYS 176
 Db 121 SWYRWFPWPGQGITLVTVSSASTKGPVPLAPSSKSTSGTAAALGCLVKDYFPPRPVYS 180
 Qy 177 WNSGALTSVHTFPFVAVLSSGLVSSVTVTPSSAFGQTATCVNDHPSNKKVDTYER 236
 Db 181 WNSGALTSVHTFPFVAVLSSGLVSSVTVTPSSAFGQTATCVNDHPSNKKVDTYER 240
 Qy 237 KCVE---CPPCPAPP-VAGPSVFLPPPKPDTLMISRTPEVTCVAVVDVSHEDPEVQFM 292
 Db 241 KSCDKTHCPCCPAPPELLGSPVFLPPPKPDTLMISRTPEVTCVAVVDVSHEDPEVQFM 300
 Qy 293 YVDGEVHNAKTKPREBQNSSTFRVSVYLAHVQDMLNGKXKCVSNKALPAPIEKTIS 352
 Db 301 YVDGEVHNAKTKPREBQNSSTFRVSVYLAHVQDMLNGKXKCVSNKALPAPIEKTIS 360
 Qy 353 KTKGPREPOVYTLPPSRBEMTKNOVSLTCLVKGFPSPDIAVWESNQGPPENNYKTTTPM 412
 Db 361 KAKGPREPOVYTLPPSRBELTKNOVSLCLVKGFPSPDIAVWESSGGPPENNYKTTTPV 420
 Qy 413 LDDSGSFFLYSKLTVDKSRMOQGNVSCSVHMEALHNHYTKSLSPGK 462
 Db 421 LDDSGSFFLYSKLTVDKSRMOQGNVSCSVHMEALHNHYTKSLSPGK 470
 RESULT 15
 O6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
 ID O6GMX1 HUMAN PRELIMINARY; PRT; 476 AA.
 AC O6GMX1
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Hypothetical protein.
 GN Name=Hypothetical protein;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Boeck S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Scherch A., Schein J.E., Jones S.J.M., Skalska U., Smalhus D.E.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

Query Match 76.7%; Score 1909; DB 2; Length 470;
 Best Local Similarity 76.8%; Pred. No. 1.1e-124;

RP NUCLEOTIDE SEQUENCE.
RC TISSUE-Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -; mRNA.
DR GO; GO:0016021; C:intricel to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-11ke.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-sec; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 76.5%; Score 1904; DB 2; Length 476;

Best Local Similarity 76.8%; Pred. No. 2, 5e-124; Matches 361; Conservative 41; Mismatches 52; Indels 16; Gaps 6;

QY 8 LFLSGTAGVISEVOIQSGPELVKPGASVKNMCKASG--YTGTDDYIHMMKSHGKSLE 65
DB 8 LLLVAPRWVLSQVQLQESGPGILVKPSQTLSLTCTVSGGISGDIYWMIRQPGKGLE 67
QY 66 WIGYIYPPNNGGNGYNOKEFGKATLTVDKSSSTAYMELRTLSBDAVYVCGRS----- 118
DB 68 WIGYIY-YSGSTYTNLSKRYTISLDTKNOPLKMSVTAADTAIVPCARAGWGGRFR 126
QY 119 TW--DFDYWGQSTLTIVSSASTKGPSVEPLAPCSRSTSESTALGCLVKDYFPBPVTVS 176
DB 127 SWAIGFNIWGGTMTVTSASSTKGPSVFPLAPSSKSTSGTALAQLVQDYFPBPVTVS 186
QY 177 WNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDRKPSNTKVDKTVR 236
DB 187 WNSGALTSGVHTFPVAVLQSSGLYSLSVTVTPSSNFGTQTYTCNVDRKPSNTKVDKTVR 246
QY 237 KCCVE---GPPCPAPP-VAGPSVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPVRQFMW 292
DB 247 KSCDKHTHTCPCPAPPELIGPSVFLPPPKDTLMISRTPEVTCVVVDVSHEDPVRQFMW 306
QY 293 YVDGVEVHNAKTPRESEGFSTFRVYSVLTVDVHQMANGKEVYCKVSNKGLPAPIRKTIS 352
DB 307 YVDGVEVHNAKTPRESEGFSTFRVYSVLTVDVHQMANGKEVYCKVSNKGLPAPIRKTIS 366
QY 353 KTKGQPREPQVYTLTPSRSEMTKNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTPPM 412
DB 367 KAKGQPREPQVYTLTPSRDELFTNQVSLTCLVKGFYPSDIAVWESNNGQPENNYKTTPPV 426
QY 413 LPSDGSFPLYSKLTVDKSRWQQGNVSCVMHEALFNHYTQKSLSLSPGK 462
DB 427 LPSDGSFPLYSKLTVDKSRWQQGNVSCVMHEALFNHYTQKSLSLSPGK 476

Search completed: January 24, 2006, 18:56:20
Job time : 152.695 secs

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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:57:25 ; Search time 22.4721 Seconds
(without alignments)
208.348 Million cell updates/sec

Title: US-10-828-782a-18

Perfect score: 2490

Sequence: 1 MEGSCVMFLPLSGTAGVLSF.....MHEALHNHYQKSLSPK 462

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70609 seqs, 10134256 residues

Total number of hits satisfying chosen parameters: 70609

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:

- 1: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/PC1_NEM_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEM_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2145.5	86.2	446	US-11-102-621-138	Sequence 138, App
2	2143.5	86.1	442	US-11-102-621-126	Sequence 126, App
3	2142.5	86.0	446	US-11-102-621-136	Sequence 136, App
4	2142.5	86.0	446	US-11-102-621-137	Sequence 137, App
5	2140.5	86.0	442	US-11-102-621-124	Sequence 124, App
6	2140.5	86.0	442	US-11-102-621-125	Sequence 125, App
7	2139.5	85.9	446	US-11-102-621-139	Sequence 139, App
8	2137.5	85.8	442	US-11-102-621-137	Sequence 127, App
9	2137.5	85.8	446	US-11-102-621-140	Sequence 140, App
10	2135.5	85.8	442	US-11-102-621-128	Sequence 128, App
11	2103.5	84.5	450	US-11-025-712-12	Sequence 12, App
12	2082	83.6	472	US-11-086-289-10	Sequence 10, App1
13	2076	83.4	464	US-11-128-900-2	Sequence 2, App1
14	2076	83.4	464	US-11-128-900-66	Sequence 66, App1
15	2074.5	83.3	444	US-11-004-590-233	Sequence 233, App
16	2072	83.2	470	US-11-144-248-45	Sequence 45, App1
17	2072	83.2	470	US-11-144-222-45	Sequence 45, App1
18	2071.5	83.2	463	US-11-128-900-4	Sequence 4, App1
19	2071.5	83.2	463	US-11-128-900-68	Sequence 68, App1
20	2069	83.1	470	US-11-144-222-49	Sequence 49, App1
21	2069	83.1	470	US-11-144-222-49	Sequence 49, App1
22	2068.5	83.1	473	US-11-144-248-50	Sequence 50, App1
23	2068.5	83.1	473	US-11-144-222-50	Sequence 50, App1
24	2067	83.0	470	US-11-144-248-46	Sequence 46, App1
25	2067	83.0	470	US-11-144-222-46	Sequence 46, App1

26	2063	82.9	472	US-11-086-289-2	Sequence 2, App1
27	2062.5	82.8	463	US-11-128-900-1	Sequence 1, App1
28	2062.5	82.8	463	US-11-128-900-63	Sequence 63, App1
29	2061.5	82.8	444	US-11-004-590-232	Sequence 232, App
30	2056.5	82.6	463	US-11-128-900-64	Sequence 64, App1
31	2056.5	82.6	471	US-11-086-289-6	Sequence 6, App1
32	2054	82.5	468	US-11-086-289-14	Sequence 14, App1
33	2052	82.4	468	US-11-086-289-22	Sequence 22, App1
34	2045	82.1	451	US-11-128-900-70	Sequence 70, App1
35	2044	82.1	470	US-11-086-289-18	Sequence 18, App1
36	2037	81.8	667	US-11-096-046-29	Sequence 29, App1
37	2035.5	81.7	467	US-11-158-505-5	Sequence 5, App1
38	2035.5	81.7	467	US-11-158-505-7	Sequence 7, App1
39	2035.5	81.7	467	US-11-158-505-21	Sequence 21, App1
40	2035.5	81.7	467	US-11-158-505-23	Sequence 23, App1
41	2032.5	81.6	471	US-11-106-820-25	Sequence 25, App1
42	2028.5	81.5	467	US-11-158-505-72	Sequence 72, App1
43	2023.5	81.3	467	US-11-158-505-13	Sequence 13, App1
44	2023.5	81.3	467	US-11-158-505-15	Sequence 15, App1
45	2023.5	81.3	467	US-11-158-505-29	Sequence 29, App1

ALIGNMENTS

RESULT 1	US-11-102-621-138	Sequence 138, Application US/11102621
;	Publication No. US20050276799A1	GENERAL INFORMATION:
;	APPLICANT: Protein Design Labs, Inc.	APPLICANT: Hinton, Paul R.
;	APPLICANT: Tsurushita, Naoya	APPLICANT: Tso, J. Yun
;	APPLICANT: Vaquez, Maximiliano	TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
;	FILE REFERENCE: 05882.0039.00PC03	CURRENT APPLICATION NUMBER: US/11/102,621
;	CURRENT FILING DATE: 2005-04-08	PRIOR APPLICATION NUMBER: US 10/822,300
;	PRIOR FILING DATE: 2004-04-09	NUMBER OF SEQ ID NOS: 146
;	SOFTWARE: PatentIn version 3.2	SEQ ID NO 138
;	LENGTH: 446	TYPE: PRT
;	ORGANISM: Homo sapiens	US-11-102-621-138
QY	20	EVQLQSSPELVKSGASVKSCKASGYGTDYTHMMKSHGKLEWIGYIPNNNGCY 79
DB	1	QVQLVQSSPELVKSGASVKSCKASGYGTDYTHMMKSHGKLEWIGYIPNNNGCY 60
QY	80	NQKKKATLTVDKSSSTAVNELRTLSSEDSAVVYCGSTWDDFD---YWGQITLVSS 136
DB	61	NQKKKATLTVDKSSSTAVNELRTLSSEDSAVVYCGSTWDDFD---YWGQITLVSS 120
QY	137	ASTGSPVFPPLAPCSRSTSESTALGCLVQYFPPEPVTVSNMGLTSGVITFPVAVLSS 196
DB	121	ASTGSPVFPPLAPCSRSTSESTALGCLVQYFPPEPVTVSNMGLTSGVITFPVAVLSS 180
QY	197	GLYSLSVTVTPSSNFGQYTCNVDPKSPSTKVDKTERKCYECPCPAPVAVPSVF 256
DB	181	GLYSLSVTVTPSSNFGQYTCNVDPKSPSTKVDKTERKCYECPCPAPVAVPSVF 240
QY	257	LPFPKPKDTLMTISRTPEVTVVVDVSHEDPEVQNMVYDGVVNAKTKPRBEQNSTFR 316
DB	241	LPFPKPKDTLMTISRTPEVTVVVDVSHEDPEVQNMVYDGVVNAKTKPRBEQNSTFR 300

Qy 317 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 376
Db 301 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 360
Qy 377 QVSLTCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQN 436
Db 361 QVSLTCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQN 420
Qy 437 VFSCSVMEBALHNNHTYOKSLSLSPGK 462
Db 421 VFSCSVMEBALHNNHTYOKSLSLSPGK 446

RESULT 2
US-11-102-621-126
; Sequence 126, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-126

Query Match 86.1%; Score 2143.5; DB 7; Length 442;
Best Local Similarity 90.1%; Pred. No. 1.4e-131;
Matches 399; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Qy 20 EVLOQSGPELVKPGASVMSCKASGYGTDYIHHMKQSHGKSLWIGIYIPNNNGNGY 79
Db 1 QVQLVQSGAEVKKPKASVSKVCSKASGYFTSYRMHWVQAPOGLWMIGIYINPSTGYTEY 60
Qy 80 NQKFKGKATLTVYDKSSSTAYMELRTLTSEDAVYTCGRSTMDPDTWGGTLLTVSSAST 139
Db 61 NQKFKDKATITADBSSTINAYMELSLRSHDTAVYTCARG-GGVFDYWGQGLTVTVSSAST 119
Qy 140 KQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSSGLY 199
Db 120 KQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSSGLY 179
Qy 200 SLSSVTVVPSNFGITQYTCNVDHKPSNTKVDKVERKCCVCEPCPAPPAAPVAGPSVFLFP 259
Db 180 SLSSVTVVPSNFGITQYTCNVDHKPSNTKVDKVERKCCVCEPCPAPPAAPVAGPSVFLFP 239
Qy 260 PRPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFRVVS 319
Db 240 PRPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFRVVS 299
Qy 320 VLTIVVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKNQVS 379
Db 300 VLTIVVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKNQVS 359
Qy 380 LITCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQNVS 439
Db 360 LITCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQNVS 419
Qy 440 CSVMHEBALHNNHTYOKSLSLSPGK 462
Db 421 CSVMHEBALHNNHTYOKSLSLSPGK 446

Db 420 CSVMHEBALHNNHTYOKSLSLSPGK 442

RESULT 3
US-11-102-621-136
; Sequence 136, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya
; APPLICANT: Tso, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCERN BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-136

Query Match 86.0%; Score 2142.5; DB 7; Length 446;
Best Local Similarity 89.7%; Pred. No. 1.7e-131;
Matches 400; Conservative 16; Mismatches 27; Indels 3; Gaps 1;

Qy 20 EVLOQSGPELVKPGASVMSCKASGYGTDYIHHMKQSHGKSLWIGIYIPNNNGNGY 79
Db 1 QVQLVQSGAEVKKPKASVSKVCSKASGYFTSYRMHWVQAPOGLWMIGIYINPSTGYTEY 60
Qy 80 NQKFKGKATLTVYDKSSSTAYMELRTLTSEDAVYTCGRSTMDPDTWGGTLLTVSSAST 136
Db 61 NQKFKDKATITADBSSTAYMELSLRSHDTAVYTCARGAAYDYDGFAYWGQGLTVTVSS 120
Qy 137 ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSS 196
Db 121 ASTKQPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVVSNMNSGALTSGVHTFPAVLQSS 180
Qy 197 GLYSLSVTVVPSNFGITQYTCNVDHKPSNTKVDKVERKCCVCEPCPAPPAAPVAGPSVFL 256
Db 181 GLYSLSVTVVPSNFGITQYTCNVDHKPSNTKVDKVERKCCVCEPCPAPPAAPVAGPSVFL 240
Qy 257 LFPKPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFR 316
Db 241 LFPKPKDTLMIKRTPEVTCVVDVSHEDPEYQFMWYVDGVEVHNAKTKPREBOFNSTFR 300
Qy 317 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 376
Db 301 VVSVLTVHODMLNGKEYCKVSNKGLPAPIEKTI SKTKGQRPBPQVYTLPPSRREMTKN 360
Qy 377 QVSLTCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQN 436
Db 361 QVSLTCLVKGFPSPDIAVWESNNGQPENNYYKTTTPMLDSDGSFFLYSKLTVDKSRWQOQN 420
Qy 437 VFSCSVMEBALHNNHTYOKSLSLSPGK 462
Db 421 VFSCSVMEBALHNNHTYOKSLSLSPGK 446

RESULT 4
US-11-102-621-137
; Sequence 137, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Tsurushita, Naoya

```

: APPLICANT: Tso, J. Yun
: APPLICANT: Vasquez, Maximiliano
: TITLE OF INVENTION: ALTERATION OF FCγR BINDING AFFINITIES OR SERUM HALF-LIVES OF
: TITLE OF INVENTION: ANTIBODIES BY MDTAGENESIS
: FILE REFERENCE: 05882.0039.00PC03
: CURRENT APPLICATION NUMBER: US/11/102,621
: CURRENT FILING DATE: 2005-04-08
: PRIOR APPLICATION NUMBER: US 10/822,300
: PRIOR FILING DATE: 2004-04-09
: NUMBER OF SEQ ID NOS: 146
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 137
: LENGTH: 446
: TYPE: PRT
: ORGANISM: Homo sapiens
US-11-102-621-137

```

Query Match	Score	DB 7	Length	446
86.0%	2142.5			

QY	20	EVOLDOOSEPELVKPAASVKMSCKASGNGCTDYVHHMKQSHKSLMEIGYIYPPNNGNCGY	79
Dp	1	QVQLVQSAEAEVKKPKASVAVKSCAKSGYFTSTYTHMVRQAPGQGLSEWVGINPRSGYTH	60
QY	80	NOKEFGKATLLTVDKSSSTAYMELRTLSHDSAAVYVCGSRITWDPD--TWGQGITLVES	136
Dp	61	NQKDKDKATLLADKASASTRAYMELSLRSRSDTAVYTCARSAAYDYDQFAWVGQGITLVES	120
QY	137	ASTKGPSVFPPLAPCRSRSTSESTALAGCLVKDYFPEPEVYVTSNMSGALTSGVHTFPAYLQSS	196
Dp	121	ASTKGPSVFPPLAPCRSRSTSESTALAGCLVKDYFPEPEVYVTSNMSGALTSGVHTFPAYLQSS	180
QY	197	GLYSLSVVTAVPSSNFGQIQTVCANDHKESNFKVDTVERKCCVCEPCPCAPAVGASPYF	256
Dp	181	GLYSLSVVTAVPSSNFGQIQTVCANDHKESNFKVDTVERKCCVCEPCPCAPAAAPSYF	240
QY	257	LPPPKPKDTLMISRTPEVYTCVVVDVSHEDPEVDQFMVYVDGVEVHNAKTYPRBEQFNSTPR	316
Dp	241	LFPKPCKDQLMISRTPEVYTCVVVDVSHEDPEVDQFMVYVDGVEVHNAKTYPRBEQFNSTPR	300
QY	317	VSVSLTVVHOMLINKEKEYKCKVSNKGLPARIKETTISKTGQPREPQVYLLPPESEEMTN	376
Dp	301	VSVSLTVVHOMLINKEKEYKCKVSNKGLPARIKETTISKTGQPREPQVYLLPPESEEMTN	360
QY	377	QVSLTCLVKGFYPSDIAVEMESNGQPRENNYKTTTPMLDSDGSFFLYSKLTVDSKRWQGN	436
Dp	361	QVSLTCLVKGFYPSDIAVEMESNGQPRENNYKTTTPMLDSDGSFFLYSKLTVDSKRWQGN	420
QY	437	VFSCGVMEHALHNHTOKSLISLSPCK	462
Dp	421	VFSCGVMEHALHNHTOKSLISLSPCK	446

RESULT 5
 US-11-102-621-124
 ; Sequence 124, Application US/11102621
 ; Publication No. US20050276799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R.
 ; APPLICANT: Teunushita, Naoya
 ; APPLICANT: Tso, J. Yun
 ; APPLICANT: Vasquez, Maximiliano
 ; TITLE OF INVENTION: ALITERATION OF FCGR BINDING AFFINITIES OR SERUM HALF-LIVES OF
 ; FILE REFERENCE: 05882.0039..00PC03
 ; CURRENT APPLICATION NUMBER: US/11/102,621
 ; CURRENT FILING DATE: 2005-04-08
 ; PRIOR APPLICATION NUMBER: US 10/822,300
 ; PRIOR FILING DATE: 2004-04-09
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn version 3.2

```

; SEQ ID NO 124
; LENGTH: 442
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-102-621-124

```

Query Match	86.0%	Score 2140.5;	DB 7;	Length 442;
Best Local Similarity	-90.1%;	Pred. No. 2.2e-131;		
Matches 399;	Conservative 17;	Mismatches 26;	Indels 1;	Gaps 1

[illegible]

```

RESULTS 6
US-11-102-621-125
Sequence 125, Application US/11102621
Publication No. US2005027679A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Hinton, Paul R.
APPLICANT: Tansuhtla, Neoya
APPLICANT: Tso, J. Yun
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: ALTERNATION OF PCRN BLENDED WITH ANTIODIES BY MUTAGENESIS
FILE REFERENCE: 05882, 0039, 00PC03
CURRENT APPLICATION NUMBER: US/11/102, 621
CURRENT FILING DATE: 2005-04-08
PRIOR APPLICATION NUMBER: US 10/822,300
PRIOR FILING DATE: 2004-04-09
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PatentIn version 3.2
SEQ ID NO 125
LENGTH: 442
TYPE: PRT
ORGANISM: Homo sapiens
US-11-102-621-125

```

Query	20	EVQLQSGPELVKPGASVKMSCKASGYNIGTYYIHMMQSHSKSLRWIGIYTPNNGNGCY	79
Query Match	86.0%;	Score 2140.5;	DB 7; Length 442;
Best Local Similarity	90.1%;	Pred. No. 2.2e-131;	
Matches 399;	Conservative 17;	Mismatches 26;	Indels 1; Gaps 1

```

Db      1 0V0LV0SAGAEVKKPSSSVKSCASGYFTSYRMHMHVROAPQGLEWIGYINPSTGYTEX 60
Qy      80 NOKFKGKATLTYDKSSSTAYMELRTLTSEDAVYTCGSRSTMDPDMGQGTTLVYSSAST 139
        61 NOKFKDKATITDEBETNTHAYMELSLRSBEDTAVYTCARG-GGVFTYMGQGTTLVYSSAST 119
Qy      140 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 199
        120 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 179
Qy      200 SLSSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 259
        180 SLSSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 239
Qy      260 PPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 319
        240 PPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 299
Qy      320 VLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 379
        300 VLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 359
Qy      380 LTCVKGFPSPDIAVEMESNGQPENNYKTTPPMLDSDGSFLYSKLTVDKSRWQQGNVFS 439
        360 LTCVKGFPSPDIAVEMESNGQPENNYKTTPPMLDSDGSFLYSKLTVDKSRWQQGNVFS 419
Qy      440 CSVMHEALHNHYTOKSLSLSPCK 462
        420 CSVMHEALHNHYTOKSLSLSPCK 442

```

RESULT 7

```

US-11-102-621-139
; Sequence 139, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Taurushita, Naoya
; APPLICANT: Teo, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-139

```

Query Match 85.9%; Score 2139.5; DB 7; Length 446;

Best Local Similarity 89.5%; Pred. No. 2,6e-131;

Matches 399; Conservative 17; Mismatches 27; Indels 3; Gaps 1;

```

Qy      20 EVYLOQSGPELVKPGASVYMSCKASGYTGTDTYYIHMKQSHGKSLIEWIGIYIPNNGNGY 79
        1 0V0LV0SAGAEVKKPSSSVKSCASGYFTSYRMHMHVROAPQGLEWIGYINPSTGYTEX 60
Qy      80 NOKFKGKATLTYDKSSSTAYMELRTLTSEDAVYTCGSRSTMDPDMGQGTTLVYSSAST 136
        61 NOKFKDKATITDEBETNTHAYMELSLRSBEDTAVYTCARG-GGVFTYMGQGTTLVYSSAST 120
Qy      120 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 196
        121 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 180

```

```

Qy      197 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 256
        181 GLYSLSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 240
Qy      257 LPPPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 316
        241 LPPPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 300
Qy      317 VVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 376
        301 VVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 360
Qy      377 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTPPMLDSDGSFLYSKLTVDKSRWQQGN 436
        361 QVSLTCLVKGFPSPDIAVEMESNGQPENNYKTTPPMLDSDGSFLYSKLTVDKSRWQQGN 420
Qy      437 VFSCSVMEALHNHYTOKSLSLSPCK 462
        421 VFSCSVMEALHNHYTOKSLSLSPCK 446

```

RESULT 8

```

US-11-102-621-127
; Sequence 127, Application US/11102621
; Publication No. US20050276799A1
; GENERAL INFORMATION:
; APPLICANT: Protein Design Labs, Inc.
; APPLICANT: Hinton, Paul R.
; APPLICANT: Taurushita, Naoya
; APPLICANT: Teo, J. Yun
; APPLICANT: Vaequez, Maximiliano
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES BY MUTAGENESIS
; FILE REFERENCE: 05882.0039.00PC03
; CURRENT APPLICATION NUMBER: US/11/102,621
; CURRENT FILING DATE: 2005-04-08
; PRIOR APPLICATION NUMBER: US 10/822,300
; PRIOR FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-102-621-127

```

Query Match 85.8%; Score 2137.5; DB 7; Length 442;

Best Local Similarity 89.8%; Pred. No. 3.4e-131;

Matches 398; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

```

Qy      20 EVYLOQSGPELVKPGASVYMSCKASGYTGTDTYYIHMKQSHGKSLIEWIGIYIPNNGNGY 79
        1 0V0LV0SAGAEVKKPSSSVKSCASGYFTSYRMHMHVROAPQGLEWIGYINPSTGYTEX 60
Qy      80 NOKFKGKATLTYDKSSSTAYMELRTLTSEDAVYTCGSRSTMDPDMGQGTTLVYSSAST 139
        61 NOKFKDKATITDEBETNTHAYMELSLRSBEDTAVYTCARG-GGVFTYMGQGTTLVYSSAST 119
Qy      140 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 199
        120 KGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNMNSGALTSGVTHFPAVLQSSGLY 179
Qy      200 SLSSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 259
        180 SLSSVTVTPSSNFGQTYTCNVDHKSNTKVDKTERKCCVCPCPAPAPALAPSVFLFP 239
Qy      260 PPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 319
        240 PPKKQTLMSIRTPETVCVVDVSHEDPEVQFMWYDGVENHNAKTKPREBOFNSTFRVVS 299
Qy      320 VLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 379
        300 VLTVVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 359

```

QY 380 LTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGNVS 439
 Db 360 LTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGNVS 419
 QY 440 CSVMHEALHNHYTKSLSPK 462
 Db 420 CSVMHEALHNHYTKSLSPK 442

RESULT 9
 US-11-102-621-140
 ; Sequence 140, Application US/11102621
 ; Publication No. US20050276799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R.
 ; APPLICANT: Tsurushita, Naoya
 ; APPLICANT: Vasequez, Maximiliano
 ; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
 ; FILE REFERENCE: 05882.0039.00PC03
 ; CURRENT FILING DATE: 2005-04-08
 ; PRIOR APPLICATION NUMBER: US 10/822,300
 ; PRIOR FILING DATE: 2004-04-09
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 140
 ; LENGTH: 446
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-102-621-140

Query Match 85.8%; Score 2137.5; DB 7; Length 446;
 Best Local Similarity 89.5%; Pred. No. 3.5e-131;
 Matches 399; Conservative 16; Mismatches 28; Indels 3; Gaps 1;

QY 20 EVOLQSGPELVKPGASVYKSCASGYGTDTYIHHMKQSHKSLKLEWGIYIPNNNGNGY 79
 Db 1 QVOLVQSGAEVKKPKASVYKSCASGYGTDTYIHHMKQSHKSLKLEWGIYIPNNNGNGY 60
 QY 80 NOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPD---YMGQGTTLTVSS 136
 Db 61 NOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPD---YMGQGTTLTVSS 120
 QY 137 ASTKGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 196
 Db 121 ASTKGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSS 180
 QY 197 GLYSLSVTVSSNFGTQTYTCNVDPKPSNTKVDKTERKCCVCEPCPCPAPPAAPSVF 256
 Db 181 GLYSLSVTVSSNFGTQTYTCNVDPKPSNTKVDKTERKCCVCEPCPCPAPPAAPSVF 240
 QY 257 LFPKPQDTMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVENNAKTKPREBOFNSTFR 316
 Db 241 LFPKPQDTMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVENNAKTKPREBOFNSTFR 300
 QY 317 VVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 376
 Db 301 VVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 360
 QY 377 QVSLTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGN 436
 Db 361 QVSLTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGN 420
 QY 437 VFGSCVMHEALHNHYTKSLSPK 462
 Db 421 VFGSCVMHEALHNHYTKSLSPK 446

RESULT 10

US-11-102-621-128
 ; Sequence 128, Application US/11102621
 ; Publication No. US20050276799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Protein Design Labs, Inc.
 ; APPLICANT: Hinton, Paul R.
 ; APPLICANT: Tsurushita, Naoya
 ; APPLICANT: Vasequez, Maximiliano
 ; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
 ; FILE REFERENCE: 05882.0039.00PC03
 ; CURRENT FILING DATE: 2005-04-08
 ; PRIOR APPLICATION NUMBER: US 10/822,300
 ; PRIOR FILING DATE: 2004-04-09
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 128
 ; LENGTH: 442
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-102-621-128

Query Match 85.8%; Score 2135.5; DB 7; Length 442;
 Best Local Similarity 89.8%; Pred. No. 4.6e-131;
 Matches 398; Conservative 17; Mismatches 27; Indels 1; Gaps 1;

QY 20 EVOLQSGPELVKPGASVYKSCASGYGTDTYIHHMKQSHKSLKLEWGIYIPNNNGNGY 79
 Db 1 QVOLVQSGAEVKKPKASVYKSCASGYGTDTYIHHMKQSHKSLKLEWGIYIPNNNGNGY 60
 QY 80 NOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPDYMGQGTTLTVSSAST 139
 Db 61 NOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPDYMGQGTTLTVSSAST 119
 QY 140 KGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSSGLY 199
 Db 120 KGPVFPPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSVHTFPAVLQSSGLY 179
 QY 200 SLSSVTVSSNFGTQTYTCNVDPKPSNTKVDKTERKCCVCEPCPCPAPPAAPSVF 259
 Db 180 SLSSVTVSSNFGTQTYTCNVDPKPSNTKVDKTERKCCVCEPCPCPAPPAAPSVF 239
 QY 260 PKPQDTMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVENNAKTKPREBOFNSTFRVVS 319
 Db 240 PKPQDTMISRTPEVTCVVVDVSHEDPEVFQNMVYDGVENNAKTKPREBOFNSTFRVVS 299
 QY 320 VLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 379
 Db 300 VLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKNQVS 359
 QY 380 LTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGNVS 439
 Db 360 LTCLVKGFPSPDIAVWESNQGPNNTKTPMLDSDSFFLYSKLTVDKSRMOQGNVS 419
 QY 440 CSVMHEALHNHYTKSLSPK 462
 Db 420 CSVMHEALHNHYTKSLSPK 442

RESULT 11
 US-11-025-712-12
 ; Sequence 12, Application US/11025712
 ; Publication No. US20050255108A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bednar, Martin M.
 ; APPLICANT: Thomas, G. Roger
 ; APPLICANT: Grose, Cordell E.
 ; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.

```

/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genetech)
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/025,712
/ FILING DATE: 28-Dec-2004
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/404,286
/ FILING DATE: 31-Mar-2003
/ APPLICATION NUMBER: 09/811384
/ FILING DATE: 20-Dec-2000
/ APPLICATION NUMBER: 09/251652
/ FILING DATE: 17-FEB-2000
/ APPLICATION NUMBER: 08/788800
/ FILING DATE: 22-JAN-1997
/ APPLICATION NUMBER: 60/093038
/ FILING DATE: 23-JAN-1996
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Evans, David W.
/ REGISTRATION NUMBER: NONE
/ REFERENCE/DOCKET NUMBER: P1729C2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/225-1739
/ TELEFAX: 650/952-9681
/
/ INFORMATION FOR SEQ ID NO: 12:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 450 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: linear
/
/ SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-11-025-712-12

Query Match      84.5%; Score 2103.5; DB 7; Length 450;
Best Local Similarity 86.5%; Pred. No. 5.4e-129;
Matches 391; Conservative 23; Mismatches 27; Indels 11; Gaps 2;

QY      20 EVLOOQSGPELVKPGASVMSCKASGTYGDIYIHMKQSHGKSLMIGIYIPNNGNGY 79
      1 EVOLVSSGGGLVQPGSGLRLSCATSGTYTETMNMNQAPGKLEWVAGINPKNGTSH 60
DB      1 NOKFKGKATLTVDKSSSTAYMEKLTITSEDNAVYYCGRSTWD-----FDYWGQGT 130
      61 NORFMDRFTISVDKSTSTAYMOMNSLRADTAVYCAR--WRGLNYGFDVRYFDWGQGT 118
QY      131 TLTVSSASTKGPSVFLAPCSRSTSRSTAALGCLVVDYFPEPYTVMNSGALITSGVHTP 190
      119 LTVSSASTKGPSVFLAPCSRSTSRSTAALGCLVVDYFPEPYTVMNSGALITSGVHTP 178
DB      191 AVLQSSGLVSLSSVTVTPSNNFTQTYTCNVDHKPSNTVVDKTVKRCCKVCEPCPAPV 250
      179 AVLQSSGLVSLSSVTVTPSNNFTQTYTCNVDHKPSNTVVDKTVKRCCKVCEPCPAPV 238
QY      251 AGPSVFLFPPKPKDTMTISRTPEVTCVVVDVSHEDPEVOFNMYVDGVYHNAKTKRBEQ 310
      239 AGPSVFLFPPKPKDTMTISRTPEVTCVVVDVSHEDPEVOFNMYVDGVYHNAKTKRBEQ 298
DB      311 FNSTFVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTISTKQPRPEQVYTLPPSR 370
      299 FNSTFVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTISTKQPRPEQVYTLPPSR 358
QY      371 EEMTKQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTPPMLDSDGSFFLYSKLTVDS 430
      359 EEMTKQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTPPMLDSDGSFFLYSKLTVDS 418
DB      431 RMOQGNVSCSVMEHALNHHYTKSLSPGK 462
QY

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DB      419 RMOQGNVSCSVMEHALNHHYTKSLSPGK 450

RESULT 12
US-11-086-289-10
/ Sequence 10, Application US/11086289
/ Publication No. US2006002929A1
/ GENERAL INFORMATION:
/ APPLICANT: KHARE, SANJAY D.
/ APPLICANT: KELLERMAN, SIRID-AIMER
/ TITLE OF INVENTION: MONOCLONAL ANTIBODIES
/ FILE REFERENCE: 06843, 0094-00000
/ CURRENT APPLICATION NUMBER: US/11/086,289
/ PRIOR FILING DATE: 2005-03-23
/ PRIOR APPLICATION NUMBER: 60/555,396
/ PRIOR FILING DATE: 2004-03-23
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 10
/ LENGTH: 472
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-086-289-10

Query Match      83.6%; Score 2082; DB 7; Length 472;
Best Local Similarity 82.2%; Pred. No. 1.4e-127;
Matches 388; Conservative 31; Mismatches 43; Indels 10; Gaps 1;

QY      1 MECSGVMLFLISGTFVSEVLOOQSGPELVKPGASVMSCKASGTYGDIYIHMKQSH 60
      1 MEFGLSWFLVALLRGVCCQVQVLSGGVQPGSLRLSCASGTFYFGMHVQAP 60
DB      61 GKSLMIGIYIPNNGANGYNOKFKATLTVDKSSSTAYMEKLTITSEDNAVYYCGRSTW 120
      61 GKGLEWAVIWDGSKNTKTAASVKGRFTISRNSKNTIYLQMSLRADTAVYCARGGY 120
QY      121 D-----DFDYWGQGTTLTVSSASTKGPSVFLAPCSRSTSRSTAALGCLVVDYF 170
      121 DVMGSVYRNSDPFDWGQGTTLTVSSASTKGPSVFLAPCSRSTSRSTAALGCLVVDYF 180
DB      171 BRYTVSNMNGALITSGVHTPFAVLQSSGLVSLSSVTVTPSNNFTQTYTCNVDHKPSNTV 230
      121 DVMGSVYRNSDPFDWGQGTTLTVSSASTKGPSVFLAPCSRSTSRSTAALGCLVVDYF 180
QY      191 BRYTVSNMNGALITSGVHTPFAVLQSSGLVSLSSVTVTPSNNFTQTYTCNVDHKPSNTV 240
      191 BRYTVSNMNGALITSGVHTPFAVLQSSGLVSLSSVTVTPSNNFTQTYTCNVDHKPSNTV 240
DB      241 DKTVERKCCVCEPCPAPVAGPSVFLFPPKPKDTMTISRTPEVTCVVVDVSHEDPEVOF 300
      241 DKTVERKCCVCEPCPAPVAGPSVFLFPPKPKDTMTISRTPEVTCVVVDVSHEDPEVOF 300
QY      291 NMYVDGVYHNAKTKRBEQFNSTFRVYSLTVVHODMLNGEKYKCKVSNKGLPAPIEKT 350
      291 NMYVDGVYHNAKTKRBEQFNSTFRVYSLTVVHODMLNGEKYKCKVSNKGLPAPIEKT 350
DB      301 NMYVDGVYHNAKTKRBEQFNSTFRVYSLTVVHODMLNGEKYKCKVSNKGLPAPIEKT 360
      301 NMYVDGVYHNAKTKRBEQFNSTFRVYSLTVVHODMLNGEKYKCKVSNKGLPAPIEKT 360
QY      351 ISKTGQPRPEQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTP 410
      351 ISKTGQPRPEQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTP 410
DB      361 ISKTGQPRPEQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTP 420
      361 ISKTGQPRPEQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMSNQGPENNYKTP 420
QY      411 PMLDSDGSFFLYSKLTVDSRMOQGNVSCSVMEHALNHHYTKSLSPGK 462
      411 PMLDSDGSFFLYSKLTVDSRMOQGNVSCSVMEHALNHHYTKSLSPGK 462
DB      421 PMLDSDGSFFLYSKLTVDSRMOQGNVSCSVMEHALNHHYTKSLSPGK 472
QY

```

RESULT 13
US-11-128-900-2

/ Sequence 2, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN B.
/ APPLICANT: HANKE, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GOREFREY

APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3
CURRENT APPLICATION NUMBER: US/11/128,900
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 10/612497
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 2003-07-01
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 09/472087
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-2

Query Match 83.4%; Score 2076; DB 7; Length 464;
Best Local Similarity 83.2%; Pred. No. 3.3e-127;
Matches 386; Conservative 31; Mismatches 45; Indels 2; Gaps 1;

QY 1 MECSGWMFLISGTAAGVLSVQLQOOSGPELVKPGASVMSCKASGYTGTDIYIHMKQSH 60
DB 1 MEFGLSWFLVALLRGVQCQVQLVESGGGVQPGISLRISCTASGFTSNYGMHWVRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNGKFKGKATLTVDKSSSTAYMELRTLSEDSAVYYC--GRS 118
DB 61 GKGLEWAVAVIYDGSNKHGDSVKRFTISDINSNTLYLQNSLRADDAVYYCARGR 120
QY 119 TWDFDVGQGTTLTVSSASATKGPSVFPPLAPCSNSTSESTAALGCLVADYPEPYTVA 178
DB 121 LGSFYDVGQGTTLTVSSASATKGPSVFPPLAPCSNSTSESTAALGCLVADYPEPYTVA 180
QY 179 SGALTSGVHTPFAVLOSGGLYSLSVTVPSNFGTQYTCNVDHKPSNTKYDKTVERKC 238
DB 181 SGALTSGVHTPFAVLOSGGLYSLSVTVPSNFGTQYTCNVDHKPSNTKYDKTVERKC 240
QY 239 CVECPCPAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGE 298
DB 241 CVECPCPAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGE 300
QY 299 VNAATKREBQFNSTFRVSVLTVDHMDLNGEKYCKVSNKGLPAPIETKISTKGP 358
DB 301 VNAATKREBQFNSTFRVSVLTVDHMDLNGEKYCKVSNKGLPAPIETKISTKGP 360
QY 359 REPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPMLDSGS 418
DB 361 REPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPMLDSGS 420
QY 419 FFLYSKLTVDKSRMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 462
DB 421 FFLYSKLTVDKSRMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 464

RESULT 14
US-11-128-900-66
Sequence 66, Application US/11128900
Publication No. US20050287136A1
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, EILEEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEORFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI DIV3
CURRENT APPLICATION NUMBER: US/11/128,900

CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: US 10/776649
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: US 10/612497
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 2003-07-01
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: US 60/113647
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 464
TYPE: PRT
ORGANISM: Homo sapiens
US-11-128-900-66

Query Match 83.4%; Score 2076; DB 7; Length 464;
Best Local Similarity 83.2%; Pred. No. 3.3e-127;
Matches 386; Conservative 31; Mismatches 45; Indels 2; Gaps 1;

QY 1 MECSGWMFLISGTAAGVLSVQLQOOSGPELVKPGASVMSCKASGYTGTDIYIHMKQSH 60
DB 1 MEFGLSWFLVALLRGVQCQVQLVESGGGVQPGISLRISCTASGFTSNYGMHWVRQAP 60
QY 61 GKSLEWIGYIYPNNGNGYNGKFKGKATLTVDKSSSTAYMELRTLSEDSAVYYC--GRS 118
DB 61 GKGLEWAVAVIYDGSNKHGDSVKRFTISDINSNTLYLQNSLRADDAVYYCARGR 120
QY 119 TWDFDVGQGTTLTVSSASATKGPSVFPPLAPCSNSTSESTAALGCLVADYPEPYTVA 178
DB 121 LGSFYDVGQGTTLTVSSASATKGPSVFPPLAPCSNSTSESTAALGCLVADYPEPYTVA 180
QY 179 SGALTSGVHTPFAVLOSGGLYSLSVTVPSNFGTQYTCNVDHKPSNTKYDKTVERKC 238
DB 181 SGALTSGVHTPFAVLOSGGLYSLSVTVPSNFGTQYTCNVDHKPSNTKYDKTVERKC 240
QY 239 CVECPCPAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGE 298
DB 241 CVECPCPAPVAGSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFMVYDGE 300
QY 299 VNAATKREBQFNSTFRVSVLTVDHMDLNGEKYCKVSNKGLPAPIETKISTKGP 358
DB 301 VNAATKREBQFNSTFRVSVLTVDHMDLNGEKYCKVSNKGLPAPIETKISTKGP 360
QY 359 REPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPMLDSGS 418
DB 361 REPQVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVWESNGQPENNYKTPPMLDSGS 420
QY 419 FFLYSKLTVDKSRMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 462
DB 421 FFLYSKLTVDKSRMQGQNVFSCSVNHEALHNHYTQKSLSLSPGK 464

RESULT 15
US-11-004-590-233
Sequence 233, Application US/11004590
Publication No. US2006000883A1
GENERAL INFORMATION:
APPLICANT: Lazar, Gregory Alan
APPLICANT: Desjardais, John R.
APPLICANT: Hammond, Phillip W.
TITLE OF INVENTION: METHODS OF GENERATING VARIANT PROTEINS WITH INCREASED HOST STRING
FILE REFERENCE: 185832/US/5
CURRENT APPLICATION NUMBER: US/11/004,590
CURRENT FILING DATE: 2004-12-03
PRIOR APPLICATION NUMBER: US 60/527,167
PRIOR FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US 60/581,613
PRIOR FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: US 60/601,665
PRIOR FILING DATE: 2004-08-13

/ PRIOR APPLICATION NUMBER: US 60/619,483
/ PRIOR FILING DATE: 2004-10-14
/ NUMBER OF SEQ ID NOS: 458
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 233
/ LENGTH: 444
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-11-004-590-233

Query Match 83.3%; Score 2074.5; DB 7; Length 444;

Best Local Similarity 86.5%; Pred. No. 3.9e-127;
Matches 386; Conservative 26; Mismatches 29; Indels 5; Gaps 3;

QY 20 EYQLQSGPELVKPGASVMSCKASGYTDTYYIHMMKSHGKSLMIGIYIPNNGNGY 79
DB 1 QIQLVQSGAEVKKPKQASVAVSCKVSGYTTSTYISWVROAPQALMMGMITYAGSNTKY 60
QY 80 NOKFKGKATLVYDKSSSTAYMEIRLTSDSAVYCGR--STMDDFDYWGQGITLVSSA 137
DB 61 SQKFGGRFVSVDTASTAYLQISLAKEDTAVYICANYGNW--FAYWGQGITLVSSA 118
QY 138 STKGSPVFPAPCSSTSTSTALGCLVQDYFPEPYTVSWSGALTSGVHTPPAVLQSSG 197
DB 119 STKGSPVFPAPCSSTSTSTALGCLVQDYFPEPYTVSWSGALTSGVHTPPAVLQSSG 178
QY 198 LYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKVERKCCVCECPCPAPP-VAGPSVF 256
DB 179 LYSLSVTVVPSNFGTQTYTCNVDHKPSNTKVDKVERKCCVCECPCPAPP-VAGPSVF 238
QY 257 LFPPKPKDTLMI SRTPPEVTCVVVDVSHEDPEVQFMWYVDGVEVHNAKTKRREQFSTFR 316
DB 239 LFPPKPKDTLMI SRTPPEVTCVVVDVSHEDPEVQFMWYVDGVEVHNAKTKRREQFSTFR 298
QY 317 VTSVLTIVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 376
DB 299 VTSVLTIVHQDWLNGKEYCKVSNKGLPAPIEKTISKTKGQPREPOVYTLPPSRREMTKN 358
QY 377 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPMLDSGSPFLYSKLTVDKSRWQGN 436
DB 359 QVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTPMLDSGSPFLYSKLTVDKSRWQGN 418
QY 437 VFSCSVMEALHNHYTQKSLSLSPGK 462
DB 419 VFSCSVMEALHNHYTQKSLSLSPGK 444

Search completed: January 24, 2006, 19:13:54
Job time : 23.4721 secs

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OM protein - protein search, using sw model

Run on: January 24, 2006, 18:56:50 ; Search time 113.021 Seconds
(without alignments)
1707.969 Million cell updates/sec

Title: US-10-828-782A-18

Perfect score: 2490
Sequence: 1 MECSVLMFLISGTAGVLSF.....MHKALHNYTKSLSPGK 462

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBSCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBSCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBSCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBSCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBSCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBSCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2490	100.0	462	US-10-828-782A-18	Sequence 18, Appl
2	2185.5	87.8	461	US-09-249-011A-24	Sequence 24, Appl
3	2174	87.3	470	US-09-859-053-28	Sequence 28, Appl
4	2174	87.3	470	US-10-800-250-28	Sequence 28, Appl
5	2174	87.3	470	US-10-625-105-28	Sequence 28, Appl
6	2172.5	87.2	471	US-10-292-088-46	Sequence 46, Appl
7	2153	86.5	464	US-10-938-353-22	Sequence 22, Appl
8	2146.5	86.2	469	US-10-835-641-23	Sequence 23, Appl
9	2146	86.2	465	US-10-910-901-12	Sequence 2, Appl
10	2145.5	86.2	462	US-10-822-300-138	Sequence 138, Appl
11	2143.5	86.1	442	US-10-822-300-126	Sequence 126, Appl
12	2143.5	86.1	469	US-11-031-485-34	Sequence 34, Appl
13	2143.5	86.0	446	US-10-822-300-136	Sequence 136, Appl
14	2142.5	86.0	446	US-10-822-300-137	Sequence 137, Appl
15	2140.5	86.0	442	US-10-822-300-113	Sequence 124, Appl
16	2140.5	86.0	442	US-10-822-300-125	Sequence 125, Appl
17	2139.5	86.0	446	US-10-822-300-117	Sequence 125, Appl
18	2139.5	85.8	442	US-10-822-300-119	Sequence 139, Appl
19	2137.5	85.8	446	US-10-822-300-140	Sequence 140, Appl
20	2137.5	85.8	469	US-11-031-485-42	Sequence 42, Appl
21	2135.5	85.8	442	US-10-822-300-118	Sequence 128, Appl
22	2128	85.5	472	US-09-301-593-30	Sequence 30, Appl
23	2128	85.5	472	US-10-159-006-30	Sequence 30, Appl
24	2127.5	85.4	461	US-11-034-655-16	Sequence 16, Appl
25	2108	84.7	445	US-10-644-277-38	Sequence 38, Appl
26	2107	84.6	445	US-10-644-277-18	Sequence 18, Appl
27	2105	84.5	445	US-10-644-277-90	Sequence 90, Appl

28	2103.5	84.5	450	US-09-811-384-12	Sequence 12, Appl
29	2103.5	84.5	450	US-10-404-286-12	Sequence 12, Appl
30	2103	84.5	445	US-10-644-277-2	Sequence 2, Appl
31	2089.5	83.9	463	US-10-656-769-34	Sequence 34, Appl
32	2088	83.9	462	US-10-910-901-14	Sequence 14, Appl
33	2086	83.8	468	US-10-723-003-12	Sequence 12, Appl
34	2086	83.8	468	US-11-004-639-12	Sequence 12, Appl
35	2086	83.8	624	US-10-723-003-30	Sequence 30, Appl
36	2086	83.8	624	US-11-004-639-30	Sequence 30, Appl
37	2086	83.8	639	US-10-723-003-32	Sequence 32, Appl
38	2086	83.8	639	US-11-004-639-32	Sequence 32, Appl
39	2084	83.7	470	US-11-013-180-4	Sequence 4, Appl
40	2084	83.7	472	US-10-006-593-67	Sequence 67, Appl
41	2084	83.7	472	US-10-307-724-67	Sequence 67, Appl
42	2084	83.7	472	US-10-737-290-67	Sequence 67, Appl
43	2076	83.4	460	US-10-938-353-26	Sequence 26, Appl
44	2076	83.4	460	US-10-938-353-74	Sequence 74, Appl
45	2076	83.4	464	US-10-153-382-9	Sequence 9, Appl

ALIGNMENTS

RESULT 1
US-10-828-782A-18
; Sequence 18, Application US/10828782A
; Publication No. US20040242848A1
; GENERAL INFORMATION:
; APPLICANT: Owens, S. Michael.
; TITLE OF INVENTION: Mouse/Human Chimeric Anti-Phencyclidine
; TITLE OF INVENTION: Antibody And Uses Thereof
; FILE REFERENCE: D6508
; CURRENT APPLICATION NUMBER: US/10/828,782A
; PRIOR FILING DATE: 2004-04-21
; PRIOR APPLICATION NUMBER: US/96/464,190
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 18
; LENGTH: 462
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of anti-PCP
; OTHER INFORMATION: ch-mab6b5 heavy chain.
US-10-828-782A-18

Query Match	100.0%; Score 2490; DB 5; Length 462;
Best Local Similarity	100.0%; Pred. No. 2.9e-166;
Matches	462; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MECSVLMFLISGTAGVLSFVQLQSGPELYKPGASVMSCKASGYGTDYIHHMKOSH 60
DB	1 MECSVLMFLISGTAGVLSFVQLQSGPELYKPGASVMSCKASGYGTDYIHHMKOSH 60
QY	61 GKSLWIGYIYIPNNGNGVNYKPKGKATLTVDKSSSTVMEKRLTSSDSAYVYGRSTW 120
DB	61 GKSLWIGYIYIPNNGNGVNYKPKGKATLTVDKSSSTVMEKRLTSSDSAYVYGRSTW 120
QY	121 DDFWVGQGTLLTVSSASTKSPVPEPLAPCSRSTSESTAAAGCLVADYFPEPVTVSNMG 180
DB	121 DDFWVGQGTLLTVSSASTKSPVPEPLAPCSRSTSESTAAAGCLVADYFPEPVTVSNMG 180
QY	181 ALTSVHTFPVAVLSSGLYSLSVTVSSNFGTQTYCNDVHKPSNKKVDTVERKCCV 240
DB	181 ALTSVHTFPVAVLSSGLYSLSVTVSSNFGTQTYCNDVHKPSNKKVDTVERKCCV 240
QY	241 ECPPEPAPVAGPSVFLPPEPKDTLMSRPEVTCVVVDVSHEDPEVQFMNVYDGVETH 300
DB	241 ECPPEPAPVAGPSVFLPPEPKDTLMSRPEVTCVVVDVSHEDPEVQFMNVYDGVETH 300
QY	301 NAKTPEEQRQNSFTFRVSVLTIVHQMINKKYEYKCKSNKGLPAPIKTIKSGQPRE 360
DB	301 NAKTPEEQRQNSFTFRVSVLTIVHQMINKKYEYKCKSNKGLPAPIKTIKSGQPRE 360

Db 301 NAKTPREBQFNSTRFVSVLTIVHODMLNGKEKCYCNKGLPAPIEKTISKTKGQPRE 360
 QY 361 POVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
 Db 361 POVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
 QY 421 LYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 462
 Db 421 LYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 462

RESULT 2
 US-09-249-011A-24
 ; Sequence 24, Application US/09249011A
 ; Patent No. US20020176855A1
 ; GENERAL INFORMATION:

APPLICANT: CO, MAN SUNG
 APPLICANT: VASQUEZ, MAXIMILIANO
 APPLICANT: CARBENO, BEATRIZ
 APPLICANT: CELINKER, ABIE CHERYL
 APPLICANT: COLLINS, MARY
 APPLICANT: GOLDMAN, SAMUEL
 APPLICANT: GRAY, GARY S.
 APPLICANT: KNIGHT, ANDREA
 APPLICANT: O'HARA, DENISE
 APPLICANT: RUP, BONITA
 APPLICANT: VELDMAN, GERTRUIDA M.
 TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
 TITLE OF INVENTION: OF TREATMENT THEREWITH
 FILE REFERENCE: 08702.0081-00000
 CURRENT APPLICATION NUMBER: US/09/249,011A
 CURRENT FILING DATE: 1999-02-12
 NUMBER OF SEQ ID NOS: 24
 SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 24
 ; LENGTH: 461
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-09-249-011A-24

Query Match 87.8%; Score 2185.5; DB 3; Length 461;

Best Local Similarity 88.5%; Pred. No. 6.6e-145; Matches 409; Conservative 19; Mismatches 33; Indels 1; Gaps 1;

QY 1 MECSQVMLFLSGTAGVLSVQLOOSGPELVKPGASVMSCKASGYTGDTYIHHMKQSH 60
 Db 1 MWMNCILFLVLTATVAGVHQVQVLSGAVKPKGSSVKKVSCASGYTFDVAICVNRQAP 60
 QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDSAVYYCGRSTW 120
 Db 61 GQGLEWIGIYINITYDNTNTNOKFKGKATLTVDKSSSTAYMELSLRSEDTAVYYCARAAW 120
 QY 121 DDFDVMGQGTTLTVSASATKGPSVFLPACSRSTSSSTALGCIYVDYPREVTVSMNG 180
 Db 121 YMDTWGQGTTLTVSASATKGPSVFLPACSRSTSSSTALGCIYVDYPREVTVSMNG 179
 QY 181 ALTSVHTPRAVLQSSGLYSLSSVTVPSNSFGTQTYTCNVDHKPSNTKVDKTVRKCVCV 240
 Db 180 ALTSVHTPRAVLQSSGLYSLSSVTVPSNSFGTQTYTCNVDHKPSNTKVDKTVRKCVCV 239
 QY 241 ECPDPCAPVAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVH 300
 Db 240 ECPDPCAPVAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVH 299
 QY 301 NAKTPREBQFNSTRFVSVLTIVHODMLNGKEKCYCNKGLPAPIEKTISKTKGQPRE 360
 Db 301 NAKTPREBQFNSTRFVSVLTIVHODMLNGKEKCYCNKGLPAPIEKTISKTKGQPRE 359
 QY 361 POVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 420
 Db 361 POVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPMLDSDGSFF 419
 QY 421 LYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 462

Db 420 LYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 461

RESULT 3
 US-09-859-053-28
 ; Sequence 28, Application US/09859053
 ; Patent No. US20020102658A1
 ; GENERAL INFORMATION:

APPLICANT: Tsuji, Takashi
 APPLICANT: Tezuka, Katsunari
 APPLICANT: Hori, No. US20020102658A1
 TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
 TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
 TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
 FILE REFERENCE: 06501-079001
 CURRENT APPLICATION NUMBER: US/09/859,053
 CURRENT FILING DATE: 2001-05-16
 PRIOR APPLICATION NUMBER: JP 2001-99508
 PRIOR FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: JP 2000-147116
 PRIOR FILING DATE: 2000-05-18
 NUMBER OF SEQ ID NOS: 43
 SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 28
 ; LENGTH: 470
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-859-053-28

Query Match 87.3%; Score 2174; DB 3; Length 470;

Best Local Similarity 86.4%; Pred. No. 4.3e-144; Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

QY 1 MECSQVMLFLSGTAGVLSVQLOOSGPELVKPGASVMSCKASGYTGDTYIHHMKQSH 60
 Db 1 MDMTRILFLVAATAGASVOVLVSGAVKPKGASVMSCKASGYTTGTGYMHVNRQAP 60
 QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDSAVYYCGRSTW 120
 Db 61 GQGLEWIMINPHSGTGYNAOKFGQRYMTMTDTSISTAYMELSRSDTAAYYCARFY 120
 QY 121 -----DDFDVMGQGTTLTVSASATKGPSVFLPACSRSTSSSTALGCIYVDYPREP 172
 Db 121 YDSGYVDADPDIWQGTMTVTVSSASTKGPSVFLPACSRSTSSSTALGCIYVDYPREP 180
 QY 173 VTVSNAGALTSGVHTPRAVLQSSGLYSLSSVTVPSNSFGTQTYTCNVDHKPSNTKVDK 232
 Db 173 VTVSNAGALTSGVHTPRAVLQSSGLYSLSSVTVPSNSFGTQTYTCNVDHKPSNTKVDK 240
 QY 233 TVERKCYCEPCAPVAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQNM 292
 Db 241 TVERKCYCEPCAPVAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVFQNM 300
 QY 293 YVDGYEVNNAKTPREBQFNSTRFVSVLTIVHODMLNGKEKCYCNKGLPAPIEKTIS 352
 Db 301 YVDGYEVNNAKTPREBQFNSTRFVSVLTIVHODMLNGKEKCYCNKGLPAPIEKTIS 360
 QY 353 KTKGQPREPOVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 412
 Db 361 KTKGQPREPOVYTLPPSRBEMTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTTPM 420
 QY 413 LQSDSFFLYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 462
 Db 421 LQSDSFFLYSKLTVDKSRMOQGNVFSQSVMHBAALHNHYTQKSLSLSPGK 470

RESULT 4
 US-10-800-250-28
 ; Sequence 28, Application US/10800250
 ; Publication No. US2004014691A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tsuji, Takashi

```
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, Nobuaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALIIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/10/800,250
CURRENT FILING DATE: 2004-03-10
PRIOR APPLICATION NUMBER: US/09/859,053
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-800-250-28

Query Match      87.3%; Score 2174; DB 4; Length 470;
Best Local Similarity 86.4%; Pred. No. 4.3e-144;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

QY 1 MECSVWMLFLISGTAGVLSVQLOOSGPELVKPGASVVMSCKASGYTGTDYYIHMKQSH 60
DB 1 MDWTWRLIFLVAANTGASHQVQLVSGAEVKKPGASVKASGYTFTGYMHVROAP 60
QY 61 GKSLIEWIGYIYPNNGGYNQKFKGKATLVYDKSSSTYMEIARTLTSEDSAVYYCGRSTW 120
DB 61 GQGLEMMGWIMPHSGTNYAQKFGQRYMTMDTSTIYMELSRISDPTAVYYCARTYY 120
QY 121 -----DDPDYWGQGTTLTVSSASTKGPSPVFLPAPCSRSTSESTALGCLVKDYFPEP 172
DB 121 YDSGGYHADPDWQGTMTVTVSSASTKGPSPVFLPAPCSRSTSESTALGCLVKDYFPEP 180
QY 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVTPSSNFGQTYTTCNVDHKPSNTKYDK 232
DB 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVTPSSNFGQTYTTCNVDHKPSNTKYDK 240
QY 233 TVERKCCVCEPCPPAPVAGPSVFLPPPKKDTLMISTRPEYTCVVDVSHEDPEVQFNW 292
DB 233 TVERKCCVCEPCPPAPVAGPSVFLPPPKKDTLMISTRPEYTCVVDVSHEDPEVQFNW 300
QY 293 YVDGVEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGKLPAPLEKTIIS 352
DB 301 YVDGVEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGKLPAPLEKTIIS 360
QY 353 KTKGQPREPOVYTLTPPSREEMTKNQVSLTCLVKGYFPSDIAVEMESNGQPENNYKTTTPPM 412
DB 361 KTKGQPREPOVYTLTPPSREEMTKNQVSLTCLVKGYFPSDIAVEMESNGQPENNYKTTTPPM 420
QY 413 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 421 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 5
US-10-625-105-28
Sequence 28, Application US/10625105
Publication No. US20040180052A1
GENERAL INFORMATION:
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, Nobuaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALIIM AND
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/10/625,105
CURRENT FILING DATE: 2003-07-22
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PRIOR APPLICATION NUMBER: US/09/859,053
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 470
TYPE: PRT
ORGANISM: Homo sapiens
US-10-625-105-28

Query Match      87.3%; Score 2174; DB 4; Length 470;
Best Local Similarity 86.4%; Pred. No. 4.3e-144;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

QY 1 MECSVWMLFLISGTAGVLSVQLOOSGPELVKPGASVVMSCKASGYTGTDYYIHMKQSH 60
DB 1 MDWTWRLIFLVAANTGASHQVQLVSGAEVKKPGASVKASGYTFTGYMHVROAP 60
QY 61 GKSLIEWIGYIYPNNGGYNQKFKGKATLVYDKSSSTYMEIARTLTSEDSAVYYCGRSTW 120
DB 61 GQGLEMMGWIMPHSGTNYAQKFGQRYMTMDTSTIYMELSRISDPTAVYYCARTYY 120
QY 121 -----DDPDYWGQGTTLTVSSASTKGPSPVFLPAPCSRSTSESTALGCLVKDYFPEP 172
DB 121 YDSGGYHADPDWQGTMTVTVSSASTKGPSPVFLPAPCSRSTSESTALGCLVKDYFPEP 180
QY 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVTPSSNFGQTYTTCNVDHKPSNTKYDK 232
DB 173 VTVSMNSGALTSGVHTFPAVALQSSGLYSLSVTVTPSSNFGQTYTTCNVDHKPSNTKYDK 240
QY 233 TVERKCCVCEPCPPAPVAGPSVFLPPPKKDTLMISTRPEYTCVVDVSHEDPEVQFNW 292
DB 233 TVERKCCVCEPCPPAPVAGPSVFLPPPKKDTLMISTRPEYTCVVDVSHEDPEVQFNW 300
QY 293 YVDGVEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGKLPAPLEKTIIS 352
DB 301 YVDGVEVNAKTKPREBOFNSTFRVSVLTVVHODMLNGKEYKCKVSNKGKLPAPLEKTIIS 360
QY 353 KTKGQPREPOVYTLTPPSREEMTKNQVSLTCLVKGYFPSDIAVEMESNGQPENNYKTTTPPM 412
DB 361 KTKGQPREPOVYTLTPPSREEMTKNQVSLTCLVKGYFPSDIAVEMESNGQPENNYKTTTPPM 420
QY 413 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 421 LDSDSGFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 470

RESULT 6
US-10-292-088-46
Sequence 46, Application US/10292088
Publication No. US2003021100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VARE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PR/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 471
TYPE: PRT
ORGANISM: Homo sapiens
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SEQUENCE DESCRIPTION: SEQ ID NO: 23;
US-10-835-641-23

Query Match 86.2%; Score 2146.5; DB 5; Length 469;
Best Local Similarity 84.9%; Pred. No. 3.6e-142;

Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

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QY 1 MECSVMFLSLAGTAVLSEVOLQOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
DB 1 MGNCSILFLVATANGVASEVOLVBSGGGLVQPGSSIALSCATSYTTEITMMHMRQAP 60
QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTW 120
DB 61 GKGLEWVAGINPKNGKGTSHQRFMDRFTISYDKSTAYMGNLSLRADTAVYYCAR--W 118
QY 121 DD-----FDWQGGTTLTVSSASTKPSVFLAPCSRSTSESTALGCLVNDYDPE 171
DB 119 RGLNGFDPVRYFDWQGGTTLTVSSASTKPSVFLAPCSRSTSESTALGCLVNDYDPE 178
QY 172 PVTSMNSGALTSGVHTFPVAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 231
DB 179 PVTSMNSGALTSGVHTFPVAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 238
QY 232 KTVERRCCVCEPCPAPVAGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVOFN 291
DB 239 KTVERRCCVCEPCPAPVAGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVOFN 298
QY 292 WYVDGVEHNAKTKREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTI 351
DB 299 WYVDGVEHNAKTKREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTI 358
QY 352 SKTKQPREPOVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 411
DB 359 SKTKQPREPOVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 418
QY 412 MLDSDGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 419 MLDSDGSFFLYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469
```

RESULT 9

US-10-910-901-2
; Sequence 2, Application US/10910901
; Publication No. US20050054019A1
; GENERAL INFORMATION:
; APPLICANT: MICHAUD, NEIL R., et al.
; TITLE OF INVENTION: ANTIBODIES TO C-MET
; FILE REFERENCE: ABX-PPS
; CURRENT APPLICATION NUMBER: US/10/910,901
; PRIOR FILING DATE: 2004-08-03
; PRIOR APPLICATION NUMBER: US 60/492,432
; PRIOR FILING DATE: 2003-08-04
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 2
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (14)
; OTHER INFORMATION: Glu or Lys
; NAME/KEY: MOD RES
; LOCATION: (42)
; OTHER INFORMATION: Ser or Thr
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (97)
; OTHER INFORMATION: Ala or Pro
US-10-910-901-2

Query Match 86.2%; Score 2146; DB 5; Length 462;

Best Local Similarity 86.8%; Pred. No. 3.9e-142;
Matches 401; Conservative 23; Mismatches 38; Indels 0; Gaps 0;

```
QY 1 MECSVMFLSLAGTAVLSEVOLQOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSH 60
DB 1 MDWMTSLIFLVAATGASVQVLQSGAEVKKPGASVMSCKASGYTTSYGFSSVNRQAP 60
QY 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTW 120
DB 61 GKSLEWIGIYIPNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTW 120
QY 61 GKGLEWVAGINPKNGKGTSHQRFMDRFTISYDKSTAYMGNLSLRADTAVYYCAR 120
DB 61 GKGLEWVAGINPKNGKGTSHQRFMDRFTISYDKSTAYMGNLSLRADTAVYYCAR 120
QY 121 DD-----FDWQGGTTLTVSSASTKPSVFLAPCSRSTSESTALGCLVNDYDPE 180
DB 121 DD-----FDWQGGTTLTVSSASTKPSVFLAPCSRSTSESTALGCLVNDYDPE 180
QY 181 ALTSGVHTFPVAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 240
DB 181 ALTSGVHTFPVAVLQSSGLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 240
QY 241 ECPPCPAPVAGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVOFNMYDGEVH 300
DB 241 ECPPCPAPVAGPSVFLPPPKDITLMISRTPEVTCVVDVSHEDPEVOFNMYDGEVH 300
QY 301 NAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTI 360
DB 301 NAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAPIEKTI 360
QY 361 POVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPMLSDGSFF 420
DB 361 POVYTLPPREEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPMLSDGSFF 420
QY 421 LYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
DB 421 LYSKLTVDKSRMQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 462
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RESULT 10

US-10-822-300-138
; Sequence 138, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTEPATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882, 0039, CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-138

Query Match 86.2%; Score 2145.5; DB 5; Length 446;
Best Local Similarity 89.7%; Pred. No. 4e-142;
Matches 400; Conservative 17; Mismatches 26; Indels 3; Gaps 1;

```
QY 20 EVOLQOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSHGKSLWIGIYIPNNGNGY 79
DB 1 QVOLQOOSGPELVKPGASVMSCKASGYTGTDYIHHMKOSHGKSLWIGIYIPNNGNGY 79
QY 80 NQKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPD--YWGQGTTLTVSS 136
DB 80 NQKFKGKATLTVDKSSSTAYMELRTLTSEDAVYCGRSTWDDPD--YWGQGTTLTVSS 136
QY 137 ASTGGSVFLAPCSRSTSESTALGCLVNDYDPEVTVPSNFGTQTYTCNVDHKPSNTKYD 196
DB 137 ASTGGSVFLAPCSRSTSESTALGCLVNDYDPEVTVPSNFGTQTYTCNVDHKPSNTKYD 196
QY 197 GLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 256
DB 197 GLYSLSVTVPSNFGTQTYTCNVDHKPSNTKYD 256
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Db      181 GLYSSTSVTVTSFSGTQTTTCNDHKSNTKVDKTVBRKCCVCEPCPPAPPAAPSVF 240
Qy      257 LPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFMVYDGVENAKTKPREEQNSTFR 316
Db      241 LPPPKDQTLMSRTPEVTCVVVDVSHEDPEVFQFMVYDGVENAKTKPREEQNSTFR 300
Qy      317 VVSUTLVHODMLNGEKYCKVSNKGLPAPIKTIKTGQPREPOVYTLPPSRREMTKN 376
Db      301 VVSUTLVHODMLNGEKYCKVSNKGLPAPIKTIKTGQPREPOVYTLPPSRREMTKN 360
Qy      377 QVSLCLVKGFPYSDIAVEMESNGOPENNYKTTTPMLDSGSPFLYSKLTVDKSRMOGN 436
Db      361 QVSLCLVKGFPYSDIAVEMESNGOPENNYKTTTPMLDSGSPFLYSKLTVDKSRMOGN 420
Qy      437 VFSQCVMEHALHNHYTQKSLSPGK 462
Db      421 VFSQCVMEHALHNHYTQKSLSPGK 446

RESULT 11
US-10-822-300-126
; Sequence 126, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patent version 3.2
; SEQ ID NO 126
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-126

Query Match      86.1%; Score 2143.5; DB 5; Length 442;
Best Local Similarity 90.1%; Pred. No. 5.5e-142;
Matches 399; Conservative 18; Mismatches 25; Indels 1; Gaps 1;

Qy      20 EYVLOOSGPELVKPGASVMSCKASGYTGTDTYIHHMKOSHGKSLKLEIGIYTPNNGNGY 79
Db      1 QVQLVQSGAEVKKPKSSVSVKSCASGYTFTSYRMHVRQAPQGLKLEIGYINPSTGYTEY 60
Qy      80 NQKFKGKATLVDSSTAYMELRTLTSEDSAVYTCGRSTWDDPDYMGQGTTLTVSSAST 139
Db      61 NQKFKDQATITLADSESTINAYMELSLRSBDIAVYTCARG-GGVFDYMGQGTTLTVSSAST 119
Qy      140 KQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 199
Db      120 KQPSVFPLAPCSRSTSESTALGCLVKDYFPEPVTVSNMGSALTSGVHTFPAVLQSSGLY 179
Qy      200 SLSSVTVTVSSNFGITQTYTCNDHKPSNTKVDKTVBRKCCVCEPCPPAPPAAPSVFLFP 259
Db      180 SLSSVTVTVSSNFGITQTYTCNDHKPSNTKVDKTVBRKCCVCEPCPPAPPAAPSVFLFP 239
Qy      260 PPKPQTLMSRTPEVTCVVVDVSHEDPEVFQFMVYDGVENAKTKPREEQNSTFRVVS 319
Db      240 PPKPQTLMSRTPEVTCVVVDVSHEDPEVFQFMVYDGVENAKTKPREEQNSTFRVVS 299
Qy      320 VLVVHODMLNGEKYCKVSNKGLPAPIKTIKTGQPREPOVYTLPPSRREMTKNQVS 379
Db      300 VLVVHODMLNGEKYCKVSNKGLPAPIKTIKTGQPREPOVYTLPPSRREMTKNQVS 359
Qy      380 LITCLVKGFPYSDIAVEMESNGOPENNYKTTTPMLDSGSPFLYSKLTVDKSRMOGNVFS 439
Db      360 LITCLVKGFPYSDIAVEMESNGOPENNYKTTTPMLDSGSPFLYSKLTVDKSRMOGNVFS 419
Qy      440 GSVMEHALHNHYTQKSLSPGK 462
Db      420 GSVMEHALHNHYTQKSLSPGK 442
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RESULT 12
US-11-031-485-34
; Sequence 34, Application US/11031485
; Publication No. US20050232917A1
; GENERAL INFORMATION:
; APPLICANT: PULLEN, NICHOLAS
; APPLICANT: MOLLOY, ELIZABETH
; APPLICANT: KELLERMAN, SIRID-AIMEE
; APPLICANT: GREEN, LARRY L.
; APPLICANT: HAAK-FRENSCHO, MARY
; TITLE OF INVENTION: ANTIBODIES TO MADCM
; FILE REFERENCE: ABX-PP6
; CURRENT APPLICATION NUMBER: US/11/031,485
; CURRENT FILING DATE: 2005-01-07
; PRIOR APPLICATION NUMBER: 60/535,490
; PRIOR FILING DATE: 2004-01-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent Ver. 3.3
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-031-485-34

Query Match      86.1%; Score 2143.5; DB 6; Length 469;
Best Local Similarity 85.9%; Pred. No. 5.9e-142;
Matches 403; Conservative 27; Mismatches 32; Indels 7; Gaps 2;

Qy      1 MECSVMTFLISGRTGVLSVQVLOOSGPELVKPGASVMSCKASGYTGTDTYIHHMKOSH 60
Db      1 MDWTMSILFLVAALAGASVOLVQSGAEVKKPKGASVSVKSCASGYTFTSYRMHVRQAP 60
Qy      61 GKSLEMGIVYIPNNGANGNOKFKGKATLVDSSTAYMELRTLTSEDSAVYTC--GR 117
Db      61 GQGLKMMGMISVYSANTYTAQVQGRVTMTADTISTYMDLRSLRSDTAIVYTCARGS 120
Qy      118 STWDDP---DYMGQGTTLTVSSASTKQPSVFPLAPCSRSTSESTALGCLVKDYFPEPV 173
Db      121 SSSGDIYYGMDVWGQGTTLTVSSASTKQPSVFPLAPCSRSTSESTALGCLVKDYFPEPV 180
Qy      174 TVSNMGSALTSGVHTFPAVLQSSGLYSLSSVTVTVSSNFGITQTYTCNDHKPSNTKVDKT 233
Db      181 TVSNMGSALTSGVHTFPAVLQSSGLYSLSSVTVTVSSNFGITQTYTCNDHKPSNTKVDKT 240
Qy      224 VERKCCVCEPCPPAPPAAPSVFLFPKPKQTLMSRTPEVTCVVVDVSHEDPEVFQFMV 293
Db      241 VERKCCVCEPCPPAPPAAPSVFLFPKPKQTLMSRTPEVTCVVVDVSHEDPEVFQFMV 300
Qy      294 VDGVEVHNAKTKPREEQNSTFRVVSVLTVHODMLNGEKYCKVSNKGLPAPIKTI9K 353
Db      301 VDGVEVHNAKTKPREEQNSTFRVVSVLTVHODMLNGEKYCKVSNKGLPAPIKTI9K 360
Qy      354 TKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPML 413
Db      361 TKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPYSDIAVEMESNGOPENNYKTTTPML 420
Qy      414 DSDGSPFLYSKLTVDKSRMOGNVFSGSVMEHALHNHYTQKSLSPGK 462
Db      421 DSDGSPFLYSKLTVDKSRMOGNVFSGSVMEHALHNHYTQKSLSPGK 469

RESULT 13
US-10-822-300-136
; Sequence 136, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRI BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
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; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 136
; LENGTH: 446
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-822-300-136
```

Query Match	86.0%;	Score 2142.5;	DB 5;	Length 446;
Best Local Similarity	89.7%;	Pred. No. 6.5e-142;		
Matches 400; Conservative	16;	Mismatches 27;	Indels 3;	Gaps 1

QY	20	EVOLQOOSPELTVKPPASVYMSCKAGYSTDYJIIHMMQSHGSKLEMIQIYIPNNGANG	79
Db	1	QVQLVQSGAEVKKRPASVYVSCSKASGYTITISTTHMVRQAPRGGLEMMGTINRSQYTH	60
QY	80	NOKEKGAATLIVDKSSSTAAMELRITLSDSAVYICGRSTWDF--YWGQSTTLTVSS	136
Db	61	NOKLDMKATLIFADKASASTAYMELSLRSESDTAVYICARSAAYYDDGPAFWGQSTTLTVSS	120
QY	137	ASTGSPAPPLAPCGRSTSESTAAIGCYKDYPRPEVTVSNMSGALTSQHTPPALQSS	196
Db	121	ASTKPSVFPPLAPCSRSTSESTAAIGCYKDYFPEPEVTVSNMSGALTSQHTPPALQSS	180
QY	197	GLYSLSSVTVVTPSSNFGIQTTCNVNDHKSNKTKVDITVERKCCVECPCPAPRVPAGPSVF	256
Db	181	GLYSLSSVTVVTPSSNFGIQTTCNVNDHKSNKTKVDITVERKCCVECPCPAPRPAALAPSVF	240
QY	257	LPPRPKQTTLMISRPEVTCTVVVDVSHEDPEVQFNATVTDGVEYHNAKTKYPRBEQFNSTER	316
Db	241	LPPRPKQDTLMISRPEVTCTVVVDVSHEDPEVQFNMYVDGVEYHNAKTKYPRBEQFNSTER	300
QY	317	VVSVLTVVHOMDLNGEKYCKVSNGLPAPIEKITISKTKGPREPOVYLLPERSREMTKN	376
Db	301	VVSVLTVVHOMDLNGEKYCKVSNKGLPAPIEKITISKTKGPREPOVYLLPERSREMTKN	360
QY	377	QVSLTCLVKGPYPSDIAVEMESNGOPENNYYKTTTPMLDSDGSFFLYSKLTVDSKRWQGN	436
Db	361	QVSLTCLVKGFYPSDIAVEMESNGOPENNYYKTTTPMLDSDGSFFLYSKLTVDSKRWQGN	420
QY	437	VFSCSVMEHALHNHTOKSLSTSPCK 462	
Db	421	VFSCSVMEHALHNHTOKSLSTSPCK 446	

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RESULT 14
US-10-822-300-137
; Sequence 137, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTEARATION OF FcRn BINDING AFFINITIES OR SERUM HALF-LIVES OF
; FILE REFERENCE: 05882.0039, CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 137
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-137

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	Query Match	Similarity	86.0%	Score	2142.5	DB 5	Length	446
Best Local	89.7%	Pred. No. 6.5e-142						
Matches	400	Conservative	16	Mismatches	27	Indels	3	Gaps
Qy	20	EVQLQDSPELTKPASPATVSMGSKASGYGTDTRYTHMKQSHGKSLSEMTGYIYNNNGNGY	79					
Db	1	QVQLVQSAEYKPKPASPATVSMGSKASGYGTDTRYTHMKVDAQPGGLEMMGYINPRGGYTHY	60					

Qy	80	IQKQFKGKXKTLIVYDSSSSSTAYAMELRFUTSEDSASVYVCGRSTWDPD--YMGGSTLLTVSS	136
Dd	61	NQKLDKDKTKTLTAADSSASTAYMELSLRSEBDIAVYICANSAYDYDQSPAYMGOSTLVTVSS	120
Qy	137	ASTGSPSVFPLAPCSGRSTSESTAAAGCLVKDYFPEPVYVSNNSGALTSGVHTPEPAVQSS	136
Dd	121	ASTGSPSVFPLAPCSGRSTSESTAAAGCLVKDYFPEPVYVSNNSGALTSGVHTPEPAVQSS	180
Qy	197	GLYSLSSTVTVTPSSNFGQTTCNCDHKPSNKKVDKTKVERKCCVECPPCPPAPVVAQPSVF	256
Dd	181	GLYSLSSTVTVTPSSNFGQTTCNCDHKPSNKKVDKTKVERKCCVECPPCPPAPVVAQPSVF	240
Qy	257	LEPPKPKDTLIMISRTPEVTCVVVDVSHEDPEVQFMNMYVDGVEVHNAAKTKPRBEQGFSTFR	316
Dd	241	LEPPKPKDTLIMISRTPEVTCVVVDVSHEDPEVQFMNMYVDGVEVHNAAKTKPRBEQGFSTFR	300
Qy	317	VVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTSKTKGQPRRPPQVYTLPPSRBEEMTKN	376
Dd	301	VVSVLTVVHODMLNGKEYKCKVSNKGLPAPIEKTSKTKGQPRRPPQVYTLPPSRBEEMTKN	360
Qy	377	QVSLTCLVKGYYPSLIAVEWESNGQRPENNYKTTTPMLDSGDSFPLYSKLTVDKSRNQGN	436
Dd	361	QVSLTCLVKGYYPSLIAVEWESNGQRPENNYKTTTPMLDSGDSFPLYSKLTVDKSRNQGN	420
Qy	437	VFSCSVMEHALHNHYTKSLSPGK	462
Dd	421	VFSCSVMEHALHNHYTKSLSPGK	446

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RESULT 15
US-10-822-300-124
; Sequence 124, Application US/10822300
; Publication No. US20050014934A1
; GENERAL INFORMATION:
; APPLICANT: Hinton, et al.
; TITLE OF INVENTION: ALTERATION OF FCRII BINDING AFFINITIES OR SERUM HALF-LIVES OF
; TITLE OF INVENTION: ANTIBODIES FOR MUTAGENESIS
; FILE REFERENCE: 05882.0039.CPUS01
; CURRENT APPLICATION NUMBER: US/10/822,300
; CURRENT FILING DATE: 2004-04-09
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-822-300-124

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	Query March	86.0%; Score 2140.5; DB 5; Length 442;
	Beet Local Similarity	90.1%; Pred. No. 8.9e-142;
	Matches 399; Conservative 17; Mismatches 26; Indels 1; Gaps 1	
Oy	20 EVOLQSSPELVKPGASVMSCKASGYGTDYIVHMKSHSKLEMIQIYPNNGANGY 79	
Dd	1 QVALVQSAAEYKKRSSYKVSCKASGYFTSTRMHWKQAPOGLEIMIGINPSTGYTEX 60	
Oy	80 NQKEKGATLLTVDSKSTAYMELRTLTSBDSAIIYCGRSTWDDFDYMGQTLLTVSSAST 139	
Dd	61 NQKFADKATITADESNTAMVELSLRSBEDTAIVYCARG-GGVFDYMGQTLLTVSSAST 119	
Oy	140 KGPSPFPLAPCSRSTSESTAALGLCYKDYFPBPPTVSNWSGALTSGVFHPAVLQSSGLY 199	
Dd	120 KGPSVFPLAPCSRSTSESTAALGLCYKDYFPBPPTVSNWSGALTSGVFHPAVLQSSGLY 179	
Oy	200 SLSSVVVPSSNFGQYTTCNVADHKBSMTXDKTVERKCVCPCPPAPPAAPSVEFLRP 259	
Dd	180 SLSSVVVPSSNFGQYTTCNVADHKPSNTXDKTVERKCVCPCPPAPPAAPSVEFLRP 239	
Oy	260 PKPKDTLMISETPYTCVVVDVSHEDPEQFNMYVDGVEVNAKTKPRBEQNSTPRVYS 319	
Dd	240 PKPKDMLMISTPEYTCVVVDVSHEDPEQFNMYVDGVEVNAKTKPRBEQNSTPRVYS 299	
Oy	320 VLTVMODMLNGEKCKCVSNKGLPAPIEKTISKTKGQPREDOVYTLPPSRBEEMTNQVS 379	

Db	300	VLTVVHODWLNKSKYCKVSNKGLPALEKTSKTKGQPREPOVYTLPPSRZEMTKNOVS	359
Qy	380	LTCLVKGFPSPDIAVWBSNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRMOQGNVFS	439
Db	360	LTCLVKGFPSPDIAVWBSNGQPENNYKTPPMLDSDGSFFLYSKLTVDKSRMOQGNVFS	419
Qy	440	CSVMHEALHNHYTOKSLSPGK	462
Db	420	CSVMHEALHNHYTOKSLSPGK	442

Search completed: January 24, 2006, 19:13:08
Job time : 114.021 secs


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Db      240 VECPCPAPAPAAVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFMVYDGVAV 299
Qy      300 HNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR 359
Db      300 HNAKTPREBOFNSTFRVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTISKTKGQPR 359
Qy      360 EPOVYTLPPSRREBMTKNQVSLTCLVKGFPSPDIAVEMESNQGPENNYKTTTPMLDSDSF 419
Db      360 EPOVYTLPPSRREBMTKNQVSLTCLVKGFPSPDIAVEMESNQGPENNYKTTTPMLDSDSF 419
Qy      420 FLYSKLTVDKSRMGOQGNVFSQVMEHALNHHTOKSLSLSPK 462
Db      420 FLYSKLTVDKSRMGOQGNVFSQVMEHALNHHTOKSLSLSPK 462

RESULT 2
US-09-859-053-28
/ Sequence 28, Application US/09859053
/ Patent No. 6803039
/ GENERAL INFORMATION:
/ APPLICANT: Teuji, Takashi
/ APPLICANT: Tezuka, Katsunari
/ APPLICANT: Hori, No. 6803039nak1
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
/ TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
/ TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
/ FILE REFERENCE: 06501-079001
/ CURRENT APPLICATION NUMBER: US/09/859,053
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: JP 2001-99508
/ PRIOR FILING DATE: 2001-03-30
/ PRIOR APPLICATION NUMBER: JP 2000-147116
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 470
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      87.3%; Score 2174; DB 2; Length 470;
Best Local Similarity 86.4%; Pred. No. 1.1e-157;
Matches 406; Conservative 25; Mismatches 31; Indels 8; Gaps 1;

Qy      1 MECSGMLFLSGTAGVLSVQLOQSGPELVKPGASVKNCSKASGYTGTDDYIHMNKQSH 60
Db      1 MDWTRILFLVLAAGAHSAQVQVLOSAGAEVKKPGASVKNCSKASGYTGTDDYIHMNRQAP 60
Qy      61 GKSLMIGIYIPNNGNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 120
Db      61 GGLMWMGINPSSGNTVAQKFGQGVMTTRDTLSISTAYMELSRILSDDTAVYCARVY 120
Qy      121 -----DDPYWGQGITLVSSASTKPSVFPPLAPCSRSTSESTALGCLVCKYFPEP 172
Db      121 -----DDPYWGQGITLVSSASTKPSVFPPLAPCSRSTSESTALGCLVCKYFPEP 180
Qy      173 VTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYCNDVHKPSNTKVDX 232
Db      181 VTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYCNDVHKPSNTKVDX 240
Qy      233 TVERRKCCVBCPPCAPPVAGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFM 292
Db      241 TVERRKCCVBCPPCAPPVAGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFM 300
Qy      293 YVDGVEVHNAKTKPREBOFNSTFRVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTIS 352
Db      301 YVDGVEVHNAKTKPREBOFNSTFRVSVLTIVHODMLNGKEYKCKVSNKGLPAPIEKTIS 360
Qy      353 KTKGQPREBOVYTLPPSRREBMTKNQVSLTCLVKGFPSPDIAVEMESNQGPENNYKTTTPM 412
Db      361 KTKGQPREBOVYTLPPSRREBMTKNQVSLTCLVKGFPSPDIAVEMESNQGPENNYKTTTPM 420

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Qy      413 LDSGSEFLYSKLTVDKSRMGOQGNVFSQVMEHALNHHTOKSLSLSPK 462
Db      421 LDSGSEFLYSKLTVDKSRMGOQGNVFSQVMEHALNHHTOKSLSLSPK 470

RESULT 3
US-07-934-373C-23
/ Sequence 23, Application US/07934373C
/ Patent No. 5821337
/ GENERAL INFORMATION:
/ APPLICANT: Paul J. Carter
/ APPLICANT: Leonard G. Presta
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 48
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Genentech, Inc.
/ STREET: 1 DNA Way
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Winpatin (Genentech)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/934,373C
/ FILING DATE: 21-Aug-1992
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lee, Wendy M.
/ REGISTRATION NUMBER: 40,378
/ REFERENCE/DOCKET NUMBER: P0709P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650/952-9881
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 469 amino acids
/ TYPE: Amino Acid
/ TOPOLOGY: Linear
US-07-934-373C-23

Query Match      86.2%; Score 2146.5; DB 1; Length 469;
Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

Qy      1 MECSGMLFLSGTAGVLSVQLOQSGPELVKPGASVKNCSKASGYTGTDDYIHMNKQSH 60
Db      1 MGSMTIILFLVATAGAHSEVQLVDSGGILVQPGSLRLSCATSGYTFEYTMHMRQAP 60
Qy      61 GKSLMIGIYIPNNGNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 120
Db      61 GKSLMIGIYIPNNGNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSBDSAVYCGRSTW 118
Qy      121 DD-----FDYWGQGITLVSSASTKPSVFPPLAPCSRSTSESTALGCLVNDYFPE 171
Db      119 RGLATGFDVRFYDVGQGITLVSSASTKPSVFPPLAPCSRSTSESTALGCLVNDYFPE 178
Qy      172 PTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYCNDVHKPSNTKVD 231
Db      179 PTVSMNSGALTSQVHTFPVAVLOSGLYSLSVTVTPSSNFGTQTYCNDVHKPSNTKVD 238
Qy      232 KTVERRKCCVBCPPCAPPVAGPSVFLFPPPKDITLMSRTPEVTCVVVDVSHEDPEVQFN 291

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Db 239 KTVRKCCVCEPCPCPAPVAGPSVFLPPPKKDTLMTSRTEVYTCVVVDVSHEDPEVQFN 298
Qy 292 WYVDGVEVHNAKTPRREQFNSTFRVYVSLTVVHODMLNGKEYCKVSNKGLPAPIEKT 351
Db 299 WYDGMVEVHNAKTPRREQFNSTFRVYVSLTVVHODMLNGKEYCKVSNKGLPAPIEKT 358
Qy 352 SKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTP 411
Db 359 SKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTP 418
Qy 412 MLDSGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHHYTKSLSPGK 462
Db 419 MLDSGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHHYTKSLSPGK 469

RESULT 4
US-08-437-642B-23
; Sequence 23, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-437-642B-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;
Best Local Similarity 84.9%; Pred No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

Qy 1 MECSCVMLFLISGAGVLSVQLQSGPELVKPGASVVMSCAKSGYTGTDYIHHMKQSH 60
Db 1 MGVMSIILFLVATAGVSVQLVSGGGLVQGGSLSLSCATSYTETETMHWNRQAP 60

Qy 61 GKSLIEWIGIYIPNNNGNGYNQKFKKATLTVDKSSSTAYMELRTLSEDSAVVYCGRSTW 120
Db 61 GKGLIEWAGINPKKGGSHNRFRMDRTISYDSTSTAYMQLBRADTAVVYCAR--W 118
Qy 121 DD-----FDYGGGTTLTSSASTKGPVPLAPCSRSTSESTALCLVYDYPE 171
Db 119 RGLNYGFDVRYFDVWGQGLTVTVSSASTKGPVPLAPCSRSTSESTALCLVYDYPE 178
Qy 172 PVTVMNSGALTSGVHTPPALQSSGLYSLSVTVVSSNGTQTCNVDHKSNTVD 231
Db 179 PVTVMNSGALTSGVHTPPALQSSGLYSLSVTVVSSNGTQTCNVDHKSNTVD 238
Qy 232 KTVRKCCVCEPCPCPAPVAGPSVFLPPPKKDTLMTSRTEVYTCVVVDVSHEDPEVQFN 291
Db 239 KTVRKCCVCEPCPCPAPVAGPSVFLPPPKKDTLMTSRTEVYTCVVVDVSHEDPEVQFN 298
Qy 292 WYVDGVEVHNAKTPRREQFNSTFRVYVSLTVVHODMLNGKEYCKVSNKGLPAPIEKT 351
Db 299 WYDGMVEVHNAKTPRREQFNSTFRVYVSLTVVHODMLNGKEYCKVSNKGLPAPIEKT 358
Qy 352 SKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTP 411
Db 359 SKTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTTP 418
Qy 412 MLDSGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHHYTKSLSPGK 462
Db 419 MLDSGSEFLYSKLTVDKSRWQGNVSCSVMEHALNHHYTKSLSPGK 469

RESULT 5
US-08-146-206C-23
; Sequence 23, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-146-206C-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;

Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

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QY 1 MECSGMFLISGTAIVSEVQLOOSGPELVKPGASVMSCKASGTYGTDYIHMKQSH 60
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Db 1 MMSGCIILFLVATATGVSEVQLVGGGLVQPGSLRLSCATSGTTFTEYHMMRQAP 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GKSLEWIGIYVNNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSDDSAVYCGRSTW 120
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GKGLEWVAGINPKNGTSHNORFMDRFTISVDKSTSTAYMOMNSLRABDTAVYYCAR--W 118
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 DD-----FDYWGQGTTLTVSSASTKGPVFPPLAPCSRSTSTALGCLVADYFPE 171
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 RGLNAGFDVRYFDVWGQGLTVSSASTKGPVFPPLAPCSRSTSTALGCLVADYFPE 178
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 172 PVTVMNSGALTSGVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 231
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 PVTVMNSGALTSGVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 238
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 232 KTVKRCCEVCPCPAPVAGPSVFLFPPKPDITMISRTPEVTCVVDVSHEDBEVOFN 291
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 KTVKRCCEVCPCPAPVAGPSVFLFPPKPDITMISRTPEVTCVVDVSHEDBEVOFN 298
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 292 WYVDGMEVHNAKTKREBQFNSTFRVSVLTVVHODMNGEKYKCKVSNKGLPADIEKTI 351
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 WYVDGMEVHNAKTKREBQFNSTFRVSVLTVVHODMNGEKYKCKVSNKGLPADIEKTI 358
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 352 SKTKQPREPOVYTLTPRSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNTKTPP 411
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 SKTKQPREPOVYTLTPRSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNTKTPP 418
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 412 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 462
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 419 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 469
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 6

US-09-705-686-23
Sequence 23, Application US/09705686
Patent No. 6639055

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.
PRESTA, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705,686

FILING DATE: 02-NOV-1993

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

APPLICATION NUMBER: 07/715272

FILING DATE: 14-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 40,378

REFERENCE/DOCKET NUMBER: P0709P1D3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1994

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 469 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-705-686-23

Query Match 86.2%; Score 2146.5; DB 2; Length 469;

Best Local Similarity 84.9%; Pred. No. 1.4e-155;

Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

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   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 GKSLEWIGIYVNNNGNGYNOKFKGKATLTVDKSSSTAYMELRTLTSDDSAVYCGRSTW 120
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 GKGLEWVAGINPKNGTSHNORFMDRFTISVDKSTSTAYMOMNSLRABDTAVYYCAR--W 118
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QY 121 DD-----FDYWGQGTTLTVSSASTKGPVFPPLAPCSRSTSTALGCLVADYFPE 171
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 RGLNAGFDVRYFDVWGQGLTVSSASTKGPVFPPLAPCSRSTSTALGCLVADYFPE 178
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 172 PVTVMNSGALTSGVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 231
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 PVTVMNSGALTSGVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKRPNTKYD 238
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 232 KTVKRCCEVCPCPAPVAGPSVFLFPPKPDITMISRTPEVTCVVDVSHEDBEVOFN 291
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 KTVKRCCEVCPCPAPVAGPSVFLFPPKPDITMISRTPEVTCVVDVSHEDBEVOFN 298
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 292 WYVDGMEVHNAKTKREBQFNSTFRVSVLTVVHODMNGEKYKCKVSNKGLPADIEKTI 351
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 WYVDGMEVHNAKTKREBQFNSTFRVSVLTVVHODMNGEKYKCKVSNKGLPADIEKTI 358
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 352 SKTKQPREPOVYTLTPRSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNTKTPP 411
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 SKTKQPREPOVYTLTPRSREMTKNQVSLTCLVKGFPYSDIAVEMESNGQPENNTKTPP 418
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 412 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 462
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 419 MUDSDGSFFLYSKLTVDKSRMOQGNVFCSCVMHEALHNHYTKSLSLSPGK 469
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RESULT 7

US-09-705-392A-23

Sequence 23, Application US/09705392A

Patent No. 671971

GENERAL INFORMATION:

APPLICANT: Carter, Paul J.

PRESTA, Leonard G.

TITLE OF INVENTION: Method for Making Humanized Antibodies

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/705,392A

FILING DATE: 02-NOV-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/146206

FILING DATE: 17-NOV-1993

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APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-705-392a-23

Query Match      86.2% Score 2146.5; DB 2; Length 469;
Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

QY 1 MECSGVMFLSTGAGVSEVLOOQSGPELVKPGASVWMSCKASGYTGDIYIHMWKSH 60
DB 1 MGWSCIILFLVATANGVSEVQVLESQGLVQPGSLRLSCATGYTFTEYTMHMRQAP 60
QY 61 GKSLKEMIGIYIPNNGNGYNOKEFGKATLTVDKSSSTAYMELRTLSEDAVYTCGRSTW 120
DB 61 GKGLKEMVAGINPKNGGTSNORFMDRFTISVDKSTSTAYMOMNSLRADTAVYYCAR--W 118
QY 121 DD-----FDWGGSTTLTVSSASTKGPSVFPPLACSRSTSTALGCLVNDYPE 171
DB 119 RGLNYGFDVRYFDWGGSTLTVSSASTKGPSVFPPLACSRSTSTALGCLVNDYPE 178
QY 172 PVTVMNSGALTSQVHTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 231
DB 179 PVTVMNSGALTSQVHTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 238
QY 232 KTVKRCCEVCPCCPAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDDEVQFN 291
DB 239 KTVKRCCEVCPCCPAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDDEVQFN 298
QY 292 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 351
DB 299 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 358
QY 332 SKTKQPREPOVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEMESNGQPPNNYKTTTP 411
DB 359 SKTKQPREPOVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEMESNGQPPNNYKTTTP 418
QY 412 MLDSDGSPFLYSKLTVDKSRWQGNVFCSVVHEALAHNYTOKSLSPGK 462
DB 419 MLDSDGSPFLYSKLTVDKSRWQGNVFCSVVHEALAHNYTOKSLSPGK 469

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RESULT 8
US-09-705-398-23

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Sequence 23, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705_398
FILING DATE: 02-NOV-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 469 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-705-398-23

Query Match      86.2% Score 2146.5; DB 2; Length 469;
Best Local Similarity 84.9%; Pred. No. 1.4e-155;
Matches 400; Conservative 27; Mismatches 33; Indels 11; Gaps 2;

QY 1 MECSGVMFLSTGAGVSEVLOOQSGPELVKPGASVWMSCKASGYTGDIYIHMWKSH 60
DB 1 MGWSCIILFLVATANGVSEVQVLESQGLVQPGSLRLSCATGYTFTEYTMHMRQAP 60
QY 61 GKSLKEMIGIYIPNNGNGYNOKEFGKATLTVDKSSSTAYMELRTLSEDAVYTCGRSTW 120
DB 61 GKGLKEMVAGINPKNGGTSNORFMDRFTISVDKSTSTAYMOMNSLRADTAVYYCAR--W 118
QY 121 DD-----FDWGGSTTLTVSSASTKGPSVFPPLACSRSTSTALGCLVNDYPE 171
DB 119 RGLNYGFDVRYFDWGGSTLTVSSASTKGPSVFPPLACSRSTSTALGCLVNDYPE 178
QY 172 PVTVMNSGALTSQVHTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 231
DB 179 PVTVMNSGALTSQVHTPPAVLQSSGLYSLSVTVVPSNFGTQYTCNVDHKPSNTKYD 238
QY 232 KTVKRCCEVCPCCPAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDDEVQFN 291
DB 239 KTVKRCCEVCPCCPAPVAGPSVFLFPKPKDITLMSRTPEVTCVVDVSHEDDEVQFN 298
QY 292 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 351
DB 299 WYVDGVEVHNAKTKPREQFNSTFRVSVLTVVHODMLNGEKYKCKVSNKGLPAIEKTI 358
QY 332 SKTKQPREPOVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEMESNGQPPNNYKTTTP 411
DB 359 SKTKQPREPOVYTLPPSRREEMTKQVSLTCLVKGFPYSDIAVEMESNGQPPNNYKTTTP 418
QY 412 MLDSDGSPFLYSKLTVDKSRWQGNVFCSVVHEALAHNYTOKSLSPGK 462
DB 419 MLDSDGSPFLYSKLTVDKSRWQGNVFCSVVHEALAHNYTOKSLSPGK 469

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RESULT 9
US-09-301-593-30

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Sequence 30, Application US/09301593a
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.

```

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/ APPLICANT: Rettig, Wolfgang U
/ TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
/ FILE REFERENCE: 0652.1890001
/ CURRENT APPLICATION NUMBER: US/09/301,593A
/ CURRENT FILING DATE: 1999-04-29
/ EARLIER APPLICATION NUMBER: EP 98107925.4
/ EARLIER FILING DATE: 1998-04-30
/ EARLIER APPLICATION NUMBER: US 60/086,049
/ EARLIER FILING DATE: 1998-05-18
/ NUMBER OF SEQ ID NOS: 108
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 30
/ LENGTH: 472
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-301-593-30

Query Match      85.5%; Score 2128; DB 2; Length 472;
Best Local Similarity 86.7%; Pred. No. 3,7e-154;
Matches 410; Conservative 20; Mismatches 31; Indels 12; Gaps 5;

QY 1 MECSQVMEFLSLGTAAGVSEVQLQDSGPFLYKPGASVKMSCKASGYTGYTHMMKQSH 60
DB 1 MMSWVFLFLSLGTAAGVSEVQLQDSGPFLYKPGASVKMSCKRTTFTETTHMMKQSH 60
QY 61 GSKLEWIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSEDAAVYCGRST- 119
DB 61 GSKLEWIGIINPNNGIPNNGKFRATLTVGKSSSTAYMELRLTSEDAAVYFCARRI 120
QY 120 ---WMD---FDYWGQTTLTSSASATKGSVPFLAPCSSTSTSTALGCLVQDPEV 173
DB 121 AVYGEHGMADYWGQSTSTVSS-STKGPSVPLPLASSKSTSGGTAALGCLVQDPEV 179
QY 174 TVSMNSGALTSQVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVD 233
DB 180 TVSMNSGALTSQVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVHKSNTKVD 239
QY 234 VERKCCV---CPKCPAP--VAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEV 289
DB 240 VERPKSCDKHTCTPCPAPFLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEV 299
QY 290 FMYVYDGVVHNAKTRREQNPSTFRVYSLTVVHODMLNGEKYCKVSNGLPAPIRK 349
DB 300 FMYVYDGVVHNAKTRREQNPSTFRVYSLTVVHODMLNGEKYCKVSNGLPAPIRK 359
QY 350 TISKTKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFFPSDIAVEMESNQGPENNYKT 409
DB 360 TISKAKGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFFPSDIAVEMESNQGPENNYKT 419
QY 410 PMLDSGGSFFLYSKLTVDKSRMVGQGVFSCSVMEBALAHNYTKSLSPGK 462
DB 420 PVLDSGGSFFLYSKLTVDKSRMVGQGVFSCSVMEBALAHNYTKSLSPGK 472

RESULT 10
PCT-US93-07832-23
/ Sequence 23, Application PC/TUS9307832
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ TITLE OF INVENTION: Immunoglobulin Variants
/ NUMBER OF SEQUENCES: 40
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genentech, Inc.
/ STREET: 460 Point San Bruno Blvd
/ CITY: South San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94080
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patin (Genentech)
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07832
/ FILING DATE: 19930820
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/715272
/ FILING DATE: 14-JUN-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/05126
/ FILING DATE: 15-JUN-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/934373
/ FILING DATE: 21-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME:
/ REGISTRATION NUMBER:
/ REFERENCE/DOCKET NUMBER: 709P2PCT
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE:
/ TELEFAX: 415/952-9881
/ TELEX: 910/371-7168
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 552 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
PCT-US93-07832-23
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Query Match 84.8%; Score 2111.5; DB 4; Length 552;

Best Local Similarity 76.8%; Pred. No. 6.2e-153; Indels 61; Gaps 3;

Matches 400; Conservative 27; Mismatches 33; Indels 61; Gaps 3;

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QY 1 MECSQVMEFLSLGTAAGVSEVQLQDSGPFLYKPGASVKMSCKASGYTGYTHMMKQSH 60
DB 34 MMSWVFLFLSLGTAAGVSEVQLQDSGPFLYKPGASVKMSCKRTTFTETTHMMKQSH 93
QY 61 GSKLEWIGIYIPNNGNGYNQKFKGKATLTVDKSSSTAYMELRTLTSEDAAVYCGRSTW 120
DB 94 GSKLEWIGIINPNNGIPNNGKFRATLTVGKSSSTAYMELRLTSEDAAVYFCARRI 151
QY 121 DD-----FDYWGQTTLTSSASATKGSVPFLAPCSSTSTSTALGCLVQDPEV 171
DB 152 RGLNATGFDVRYFDYWGQTLTVSSASATKGSVPFLAPCSSTSTSTALGCLVQDPEV 211
QY 172 TVSMNSGALTSQVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVDHKPSNTKVD 231
DB 212 PTVSMNSGALTSQVHTFPAYLQSSGLYSLSVTVTPSSNFGTQTYTCNVHKSNTKVD 271
QY 232 KTVERRKCV-----E 241
DB 272 KTVERRKCVTCPCPAPFLGSPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEV 331
QY 242 CPKCPAPVAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVPMVVDGVEVHN 301
DB 332 CPKCPAPVAGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVPMVVDGVEVHN 391
QY 302 AKTKREQNPSTFRVYSLTVVHODMLNGEKYCKVSNGLPAPIRKISTKQPREP 361
DB 392 AKTKREQNPSTFRVYSLTVVHODMLNGEKYCKVSNGLPAPIRKISTKQPREP 451
QY 362 QVYTLPPSRREMTKNQVSLTCLVKGFFPSDIAVEMESNQGPENNYKTTPMMLDSGGSF 421
DB 452 QVYTLPPSRREMTKNQVSLTCLVKGFFPSDIAVEMESNQGPENNYKTTPMMLDSGGSF 511
QY 422 YSKLTVDKSRMVGQGVFSCSVMEBALAHNYTKSLSPGK 462
DB 512 YSKLTVDKSRMVGQGVFSCSVMEBALAHNYTKSLSPGK 552
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RESULT 11
US-08-788-800-12
/ Sequence 12, Application US/08788800
/ Patent No. 5914112

```

GENERAL INFORMATION:
APPLICANT: Bednar, Martin M.
APPLICANT: Thomas, G. Roger
APPLICANT: Gross, Cordell E.
TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,800
FILING DATE: 22-Jan-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0987-1
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-788-800-12

Query Match      84.5%; Score 2103.5; DB 1; Length 450;
Best Local Similarity 86.5%; Pred. No. 2,6e-152;
Matches 391; Conservative 23; Mismatches 27; Indels 11; Gaps 2;

QY 20 EVLOQSGPELVKPGASVMSCKASGYGTDYIYHMKQSHKSLSEWIGYIPNNGANGY 79
DB 1 EVOLVESGGGLVQPGSIRLSGATGTYFTETVTHMMQAPKGLFWAGINPKKNGTSH 60
QY 80 NQKFKGKATLVNKKSSSTAYNELRTLTSBDSAVYCGSTWMD-----FDYWGQGT 130
DB 61 NQKFKGKATLVNKKSSSTAYNELRTLTSBDSAVYCGSTWMD-----FDYWGQGT 118
QY 131 TLTVSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVYVSNMGLTSGVHP 190
DB 119 LVTSSASTKGPSPVPLAPCSRSTSESTALGCLVKDYFPEPVYVSNMGLTSGVHP 178
QY 191 AVLOSGGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVKRCCECPPEAPPV 250
DB 179 AVLOSGGLYSLSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVKRCCECPPEAPPV 238
QY 251 AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFMNYVDGVENNAKTRPEEQ 310
DB 239 AGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFMNYVDGVENNAKTRPEEQ 298
QY 311 FNSTRTVVSVLTIVHQDMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 370
DB 299 FNSTRTVVSVLTIVHQDMLNGEKYCKVSNKGLPAPIEKTISKTKGQPREPQVYTLPPSR 358
QY 371 EEMTKNQVSLTCLVGFYPSDIAVEMESNGQPENNYKTPPMLDSDGSFPLYSKLTIVKS 430
DB 359 EEMTKNQVSLTCLVGFYPSDIAVEMESNGQPENNYKTPPMLDSDGSFPLYSKLTIVKS 418
QY 431 RMQOGNVFSCSVHMAHLNHYTQKSLISLSPGK 462
DB 419 RMQOGNVFSCSVHMAHLNHYTQKSLISLSPGK 450

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RESULT 12
US-09-238-741-4
Sequence 4, Application US/09238741
Patent No. 6897044
GENERAL INFORMATION:
APPLICANT: BRASLAWSKY, GARY R.
APPLICANT: HANNA, NABIL
APPLICANT: HARIHARAN, KANDASAMY
APPLICANT: LABAREE, MICHAEL J.
APPLICANT: HUTNH, TRI B.
TITLE OF INVENTION: PRODUCTION OF TETRAVALENT ANTIBODIES
FILE REFERENCE: 23522,0584
CURRENT APPLICATION NUMBER: US/09/238,741
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 4
LENGTH: 470
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: "Dimeric" Anti-CD20 Heavy Chain (Version 1)
US-09-238-741-4

Query Match      83.7%; Score 2084; DB 2; Length 470;
Best Local Similarity 84.0%; Pred. No. 8.3e-151;
Matches 395; Conservative 27; Mismatches 40; Indels 8; Gaps 3;

QY 1 MECSVMLFLTSGTAGVLSVLOLOQSGPELVKPGASVMSCKASGYGTDYIYHMKQSH 60
DB 1 MGSMLTLLFLVAVATRVLSVLOLOQSGPELVKPGASVMSCKASGYGTDYIYHMKQSH 60
QY 61 GKSLEWIGYIPNNGANGYNQKFKGKATLVNKKSSSTAYNELRTLTSBDSAVYCGSTW 120
DB 61 GRGLEWIGYIPNNGANGYNQKFKGKATLVNKKSSSTAYNELRTLTSBDSAVYCGSTW 120
QY 121 DD---FPMWQGTITLTYSASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVYVS 176
DB 121 YGDGMVFNWAGATVTVSAASTKGPSVPLAPCSRSTSESTALGCLVKDYFPEPVYVS 180
QY 177 MNSGLTSGVTPFPAVLDSGLYSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVK 236
DB 181 MNSGLTSGVTPFPAVLDSGLYSVTVTPSSNFGTQTYTCNVDHKSNKTKVDKTVK 240
QY 237 KCVE---CPKCPAPV-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFM 292
DB 241 KSCDKHTKCPKCPAPV-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFM 300
QY 293 YVDGVEVNAKTRPEEQFNSTFRVSVLTIVHQDMLNGEKYCKVSNKGLPAPIEKTIS 352
DB 301 YVDGVEVNAKTRPEEQFNSTFRVSVLTIVHQDMLNGEKYCKVSNKGLPAPIEKTIS 360
QY 353 KTKGQPREPQVYTLPPSRSEEMTKNQVSLTCLVGFYPSDIAVEMESNGQPENNYKTPP 412
DB 361 KAKGQPREPQVYTLPPSRSEEMTKNQVSLTCLVGFYPSDIAVEMESNGQPENNYKTPP 420
QY 413 LDSDSFPLYSKLTIVDKSRMVOGNAVFSQVHMAHLNHYTQKSLISLSPGK 462
DB 421 LDSDSFPLYSKLTIVDKSRMVOGNAVFSQVHMAHLNHYTQKSLISLSPGK 470

RESULT 13
US-09-472-087-2
Sequence 2, Application US/09472087
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, BILLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.

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Qy 21 VOLQOSGBELVKGASVVMSCASGYTGTDDYIHHMKOSHGLMIGIYIYNNNGNGYN 80
Db 1 VOLQOSGBELVKGASVVMSCASGYTGTDDYIHHMKOSHGLMIGIYIYNNNGNGYN 60
Qy 81 QKFKGKATLTVDKSSSTAAMELRLTJSEDSAVYCGRST---WDD---FDYWGQTTLT 133
Db 61 QKFKGKATLTVDKSSSTAAMELRLTJSEDSAVYFCARRIAVGYDEGHAMDYWGQTSVT 120
Qy 134 VSSASTKGPSPVPLAPCSRSTSESTAALGCLVKOYFPPRPTVYVSNWNGALTSQVHTFPAYL 193
Db 121 VSSASTKGPSPVPLAPCSRSTSESTAALGCLVKOYFPPRPTVYVSNWNGALTSQVHTFPAYL 180
Qy 194 QSSGLYSLSVYTVPSNFGTQTYTCNDHKPSNTKVDKVERKCCVE---CPPCPAPP- 249
Db 181 QSSGLYSLSVYTVPSNFGTQTYTCNDHKPSNTKVDKVERKCCVE---CPPCPAPP- 240
Qy 250 VAGPSVFLPPPKXDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGYEVHNAKTKPREE 309
Db 241 LGPSVFLPPPKXDTLMISRTPEVTCVVDVSHEDPEVQFNWYVDGYEVHNAKTKPREE 300
Qy 310 QPNSTFRVSVLTIVHOMLNKKEYKCVSNKGLPAPIEKTISKTKGQPREPOVYTTLPSS 369
Db 301 QPNSTFRVSVLTIVHOMLNKKEYKCVSNKGLPAPIEKTISKTKGQPREPOVYTTLPSS 360
Qy 370 REEMTKNOVSLTCLVKGFPSPDIAYEWSNGOPENNKTTPMLDSDGSPFLYSKLTVDK 429
Db 361 REEMTKNOVSLTCLVKGFPSPDIAYEWSNGOPENNKTTPMLDSDGSPFLYSKLTVDK 420
Qy 430 SRMOQGNVFCSCVMHEALHNHYTKSLSPGK 462
Db 421 SRMOQGNVFCSCVMHEALHNHYTKSLSPGK 453
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Search completed: January 24, 2006, 18:58:34
Job time : 43.6395 secs

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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